

FIG. 1A

5'			11			20			29			38			47			56
	GAG	ACT	CAC	GGT	CAA	GCT	AAG	GCG	AAG	AGT	GGG	TGG	CTG	AAG	CCA	TAC	TAT	TTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			65			74			83			92			101			110
	ATA	GAA	TTA	ATG	GAA	AGC	AGA	AAA	GAC	ATC	ACA	AAC	CAA	GAA	GAA	CTT	TGG	AAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
				M	E	S	R	K	D	I	T	N	Q	E	E	L	W	K
			119			128			137			146			155			164
	ATG	AAG	CCT	AGG	AGA	AAT	TTA	GAA	GAA	GAC	GAT	TAT	TTG	CAT	AAG	GAC	ACG	GGA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	M	K	P	R	R	N	L	E	E	D	D	Y	L	H	K	D	T	G
			173			182			191			200			209			218
	GAG	ACC	AGC	ATG	CTA	AAA	AGA	CCT	GTG	CTT	TTG	CAT	TTG	CAC	CAA	ACA	GCC	CAT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	E	T	S	M	L	K	R	P	V	L	L	H	L	H	Q	T	A	H
			227			236			245			254			263			272
	GCT	GAT	GAA	TTT	GAC	TGC	CCT	TCA	GAA	CTT	CAG	CAC	ACA	CAG	GAA	CTC	TTT	CCA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	A	D	E	F	D	C	P	S	E	L	Q	H	T	Q	E	L	F	P
			281			290			299			308			317			326
	CAG	TGG	CAC	TTG	CCA	ATT	AAA	ATA	GCT	GCT	ATT	ATA	GCA	TCT	CTG	ACT	TTT	CTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	<u>Q</u>	<u>W</u>	<u>H</u>	<u>L</u>	<u>P</u>	<u>I</u>	<u>K</u>	<u>I</u>	<u>A</u>	<u>A</u>	<u>I</u>	<u>I</u>	<u>A</u>	<u>S</u>	<u>L</u>	<u>T</u>	<u>F</u>	<u>L</u>
			335			344			353			362			371			380
	TAC	ACT	CTT	CTG	AGG	GAA	GTA	ATT	CAC	CCT	TTA	GCA	ACT	TCC	CAT	CAA	CAA	TAT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	<u>Y</u>	<u>T</u>	<u>L</u>	<u>L</u>	R	E	V	I	H	P	L	A	T	S	H	Q	Q	Y
			389			398			407			416			425			434
	TTT	TAT	AAA	ATT	CCA	ATC	CTG	GTC	ATC	AAC	AAA	GTC	TTG	CCA	ATG	GTT	TCC	ATC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	F	Y	K	I	P	I	L	V	<u>I</u>	<u>N</u>	<u>K</u>	<u>V</u>	<u>L</u>	<u>P</u>	<u>M</u>	<u>V</u>	<u>S</u>	<u>I</u>
			443			452			461			470			479			488
	ACT	CTC	TTG	GCA	TTG	GTT	TAC	CTG	CCA	GGT	GTG	ATA	GCA	GCA	ATT	GTC	CAA	CTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	<u>T</u>	<u>L</u>	<u>L</u>	<u>A</u>	<u>L</u>	<u>V</u>	<u>Y</u>	<u>L</u>	<u>P</u>	<u>G</u>	<u>V</u>	<u>I</u>	<u>A</u>	A	I	V	Q	L
			497			506			515			524			533			542
	CAT	AAT	GGA	ACC	AAG	TAT	AAG	AAG	TTT	CCA	CAT	TGG	TTG	GAT	AAG	TGG	ATG	TTA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	H	N	G	T	K	Y	K	K	F	P	H	W	L	D	K	W	M	L
			551			560			569			578			587			596
	ACA	AGA	AAG	CAG	TTT	GGG	CTT	CTC	AGT	TTC	TTT	TTT	GCT	GTA	CTG	CAT	GCA	ATT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	T	R	K	<u>Q</u>	<u>F</u>	<u>G</u>	<u>L</u>	<u>L</u>	<u>S</u>	<u>F</u>	<u>F</u>	<u>F</u>	<u>A</u>	<u>V</u>	<u>L</u>	<u>H</u>	<u>A</u>	<u>I</u>
			605			614			623			632			641			650
	TAT	AGT	CTG	TCT	TAC	CCA	ATG	AGG	CGA	TCC	TAC	AGA	TAC	AAG	TTG	CTA	AAC	TGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	<u>Y</u>	<u>S</u>	<u>L</u>	<u>S</u>	<u>Y</u>	<u>P</u>	<u>M</u>	R	R	S	Y	R	Y	K	L	L	N	W

GCA	TAT	659	CAA	CAG	GTC	668	CAA	CAA	AAT	677	AAA	GAA	GAT	686	GCC	TGG	ATT	695	GAG	CAT	GAT	704	GTT
A	Y	Q	Q	V	Q	Q	N	K	E	D	A	W	I	E	H	D	V						
TGG	AGA	713	ATG	GAG	ATT	722	TAT	GTG	TCT	731	CTG	GGA	ATT	740	GTG	GGA	TTG	749	GCA	ATA	CTG	758	GCT
W	R	M	E	I	<u>Y</u>	<u>V</u>	<u>S</u>	<u>L</u>	<u>G</u>	<u>I</u>	<u>V</u>	<u>G</u>	<u>L</u>	<u>A</u>	<u>I</u>	<u>L</u>	<u>A</u>						
CTG	TTG	767	GCT	GTG	ACA	776	TCT	ATT	CCA	785	TCT	GTG	AGT	794	GAC	TCT	TTG	803	ACA	TGG	AGA	812	GAA
<u>L</u>	<u>L</u>	<u>A</u>	<u>V</u>	<u>T</u>	<u>S</u>	<u>I</u>	<u>P</u>	<u>S</u>	<u>V</u>	S	D	S	L	T	W	R	E						
TTT	CAC	821	TAT	ATT	CAG	830	AGC	AAG	CTA	839	GGA	ATT	GTT	848	TCC	CTT	CTA	857	CTG	GGC	ACA	866	ATA
F	H	Y	I	<u>Q</u>	<u>S</u>	<u>K</u>	<u>L</u>	<u>G</u>	<u>I</u>	<u>V</u>	<u>S</u>	<u>L</u>	<u>L</u>	<u>L</u>	<u>G</u>	<u>T</u>	<u>I</u>						
CAC	GCA	875	TTG	ATT	TTT	884	GCC	TGG	AAT	893	AAG	TGG	ATA	902	GAT	ATA	AAA	911	CAA	TTT	GTA	920	TGG
<u>H</u>	<u>A</u>	<u>L</u>	<u>I</u>	<u>F</u>	<u>A</u>	<u>W</u>	<u>N</u>	<u>K</u>	W	I	D	I	K	Q	F	V	W						
TAT	ACA	929	CCT	CCA	ACT	938	TTT	ATG	ATA	947	GCT	GTT	TTC	956	CTT	CCA	ATT	965	GTT	GTC	CTG	974	ATA
Y	T	P	P	T	F	<u>M</u>	<u>I</u>	<u>A</u>	<u>V</u>	<u>F</u>	<u>L</u>	<u>P</u>	<u>I</u>	<u>V</u>	<u>V</u>	<u>L</u>	<u>I</u>						
TTT	AAA	983	AGC	ATA	CTA	992	TTC	CTG	CCA	1001	TGC	TTG	AGG	1010	AAG	AAG	ATA	1019	CTG	AAG	ATT	1028	AGA
<u>F</u>	<u>K</u>	<u>S</u>	<u>I</u>	<u>L</u>	<u>F</u>	<u>L</u>	<u>P</u>	<u>C</u>	<u>L</u>	R	K	K	I	L	K	I	R						
CAT	GGT	1037	TGG	GAA	GAC	1046	GTC	ACC	AAA	1055	ATT	AAC	AAA	1064	ACT	GAG	ATA	1073	TGT	TCC	CAG	1082	TTG
H	G	W	E	D	V	T	K	I	N	K	T	E	I	C	S	Q	L						
TAG	AAT	1091	TAC	TGT	TTA	1100	CAC	ACA	TTT	1109	TTG	TTC	AAT	1118	ATT	GAT	ATA	1127	TTT	TAT	CAC	1136	CAA
*	N	Y	C	L	H	T	F	L	F	N	I	D	I	F	Y	H	Q						
CAT	TTC	1145	AAG	TTT	GTA	1154	TTT	GTT	AAT	1163	AAA	ATG	ATT	1172	ATT	CAA	GGA	1181	AAA	AAA	AAA	1190	AAA
H	F	K	F	V	F	V	N	K	M	I	I	Q	G	K	K	K	K						

AAA AA 3'

K

FIG. 1B

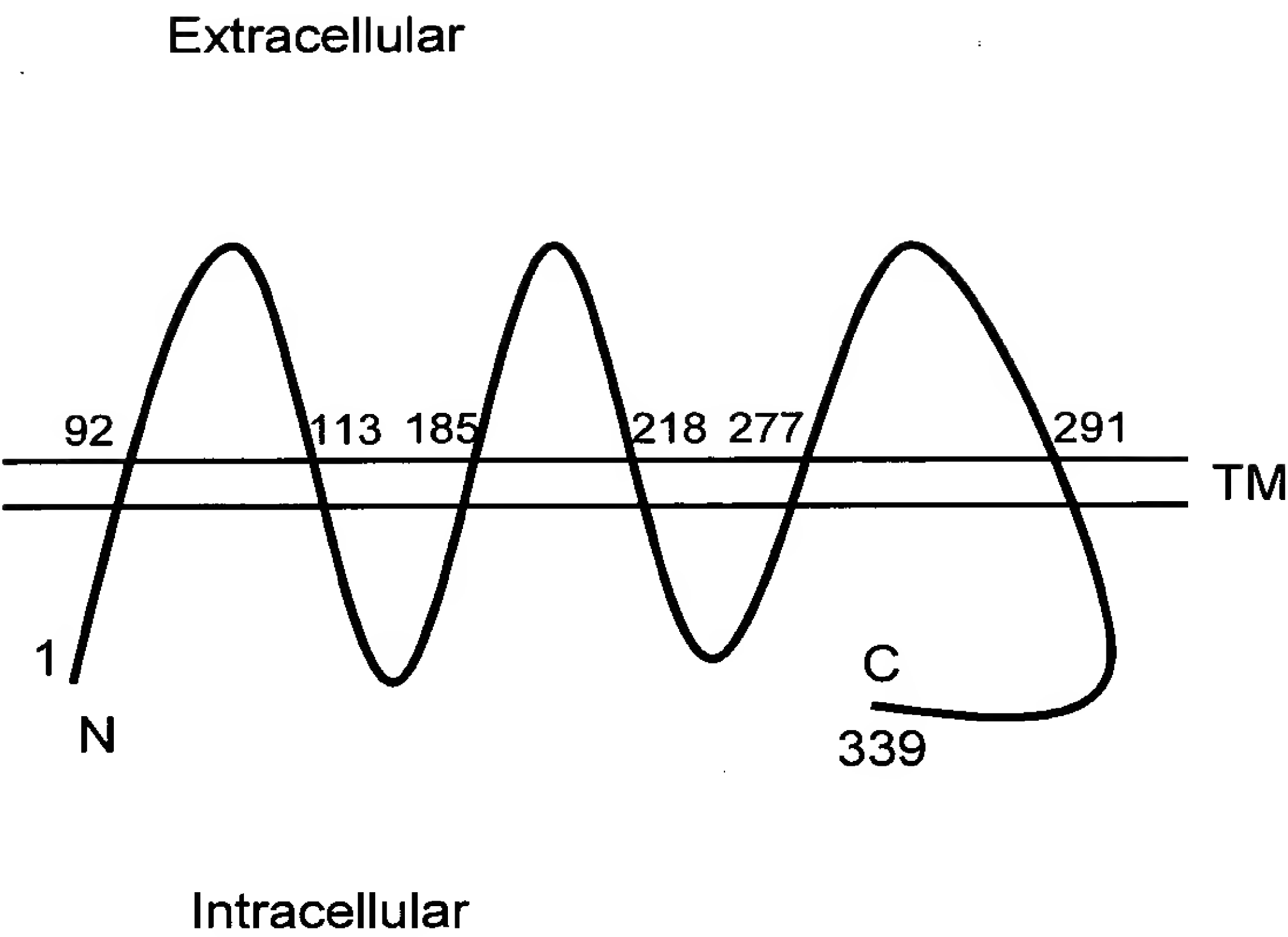
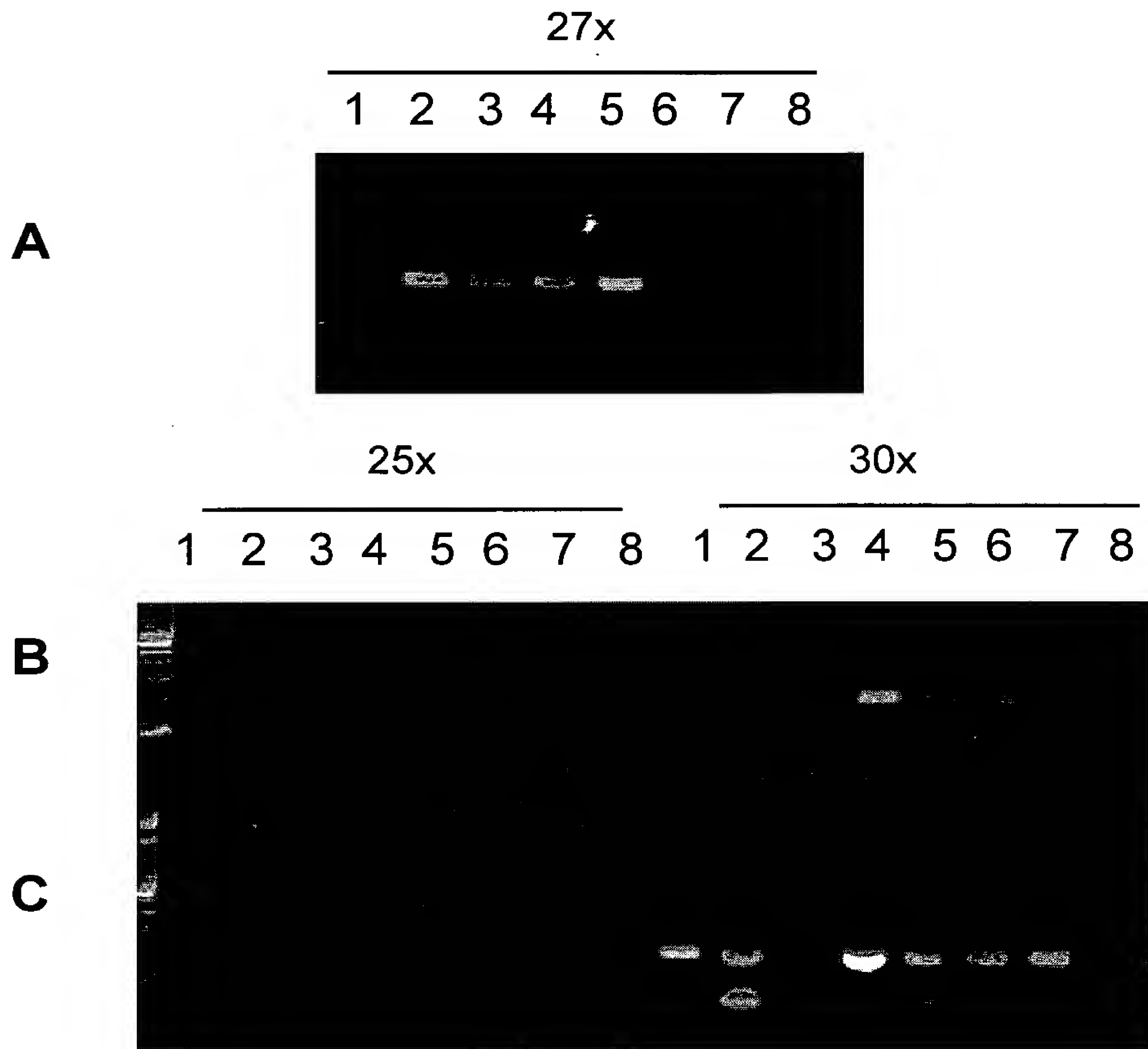


FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3'

FIG. 2



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

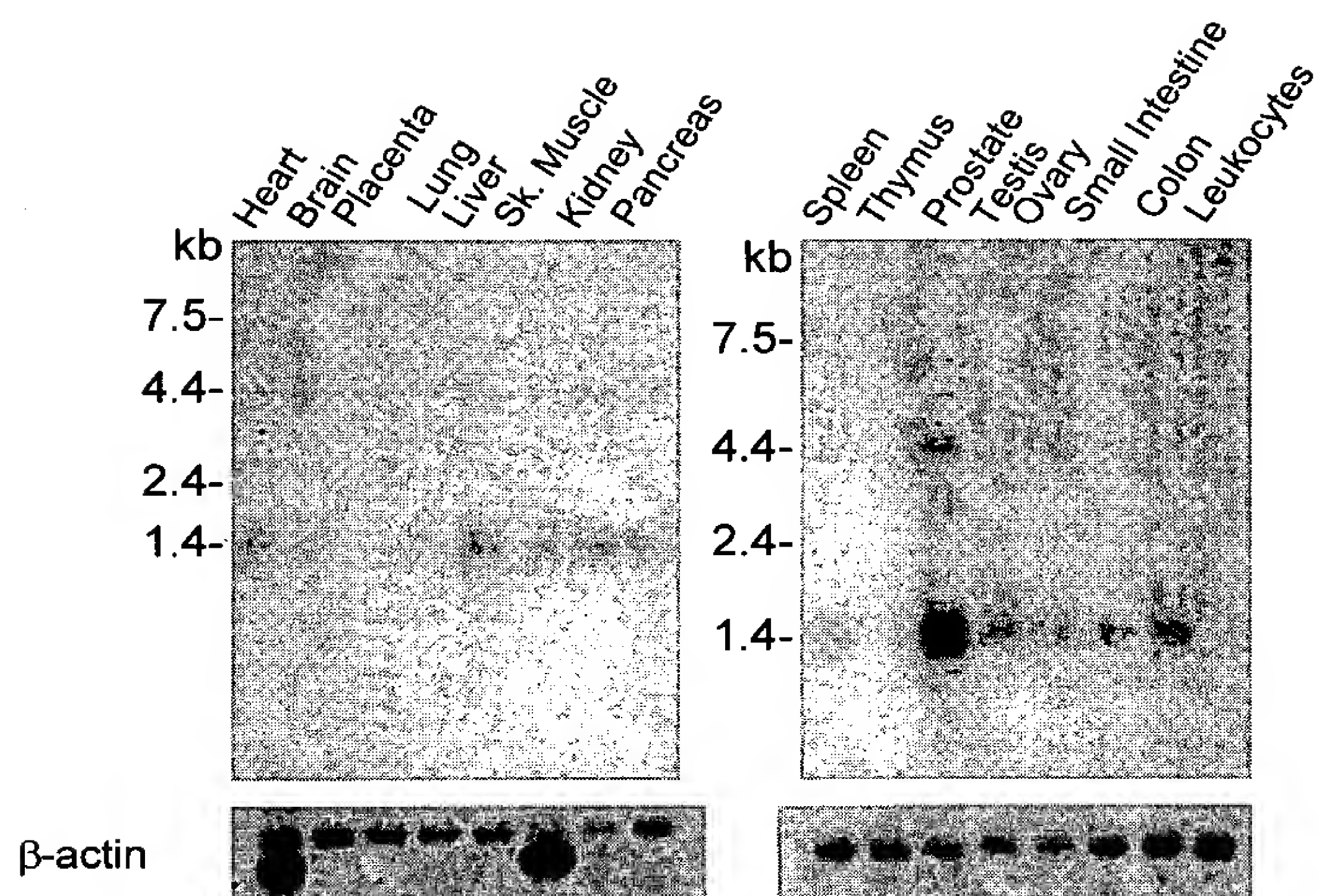


FIG. 3B

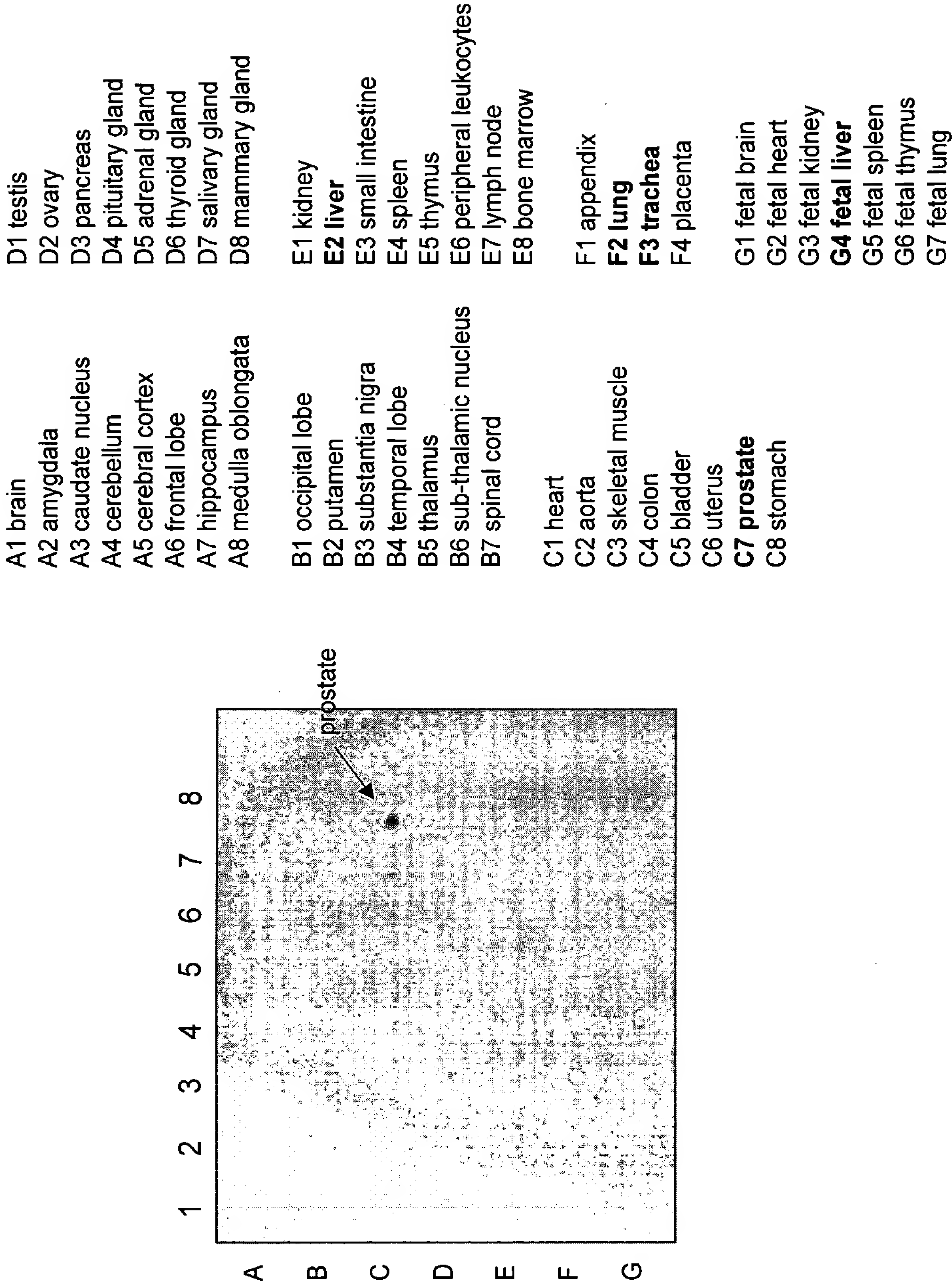


FIG. 4

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA
GTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATAACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG
AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCOAATT
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAAGGCAT
TAAAATATTCTTTGTTTTTTTTTTTTTTGTTTGTTTGTTTTTTGTTTGTTTGTTTGTTTTTTTGAGATGAAGTCTCG
CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAAGGCGATTCT
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTTAGTA
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT
GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACC
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTTCCAGAAACAAAACTCTCTCCTTGAAA
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTAATTTTGTAGGTTTCAG
CCTGATAACCACTGGAGTTCCTTGGTCCTCATTAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA
TGAACACTGCTTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTACA

ATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAACTAATTTTCAACCAATGACATGTATTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA
ACGCAAACCTTAGCTATTTGATTGTATTCACCTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT
TGAGATTACATAGGTGAACAACCTATTTTAAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCAATTTATCAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACCTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG
TTCACCTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCCTGATATTTAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAATTAACAAAACCTGAG
ATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCAACATTTCA
AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA

FIG. 5

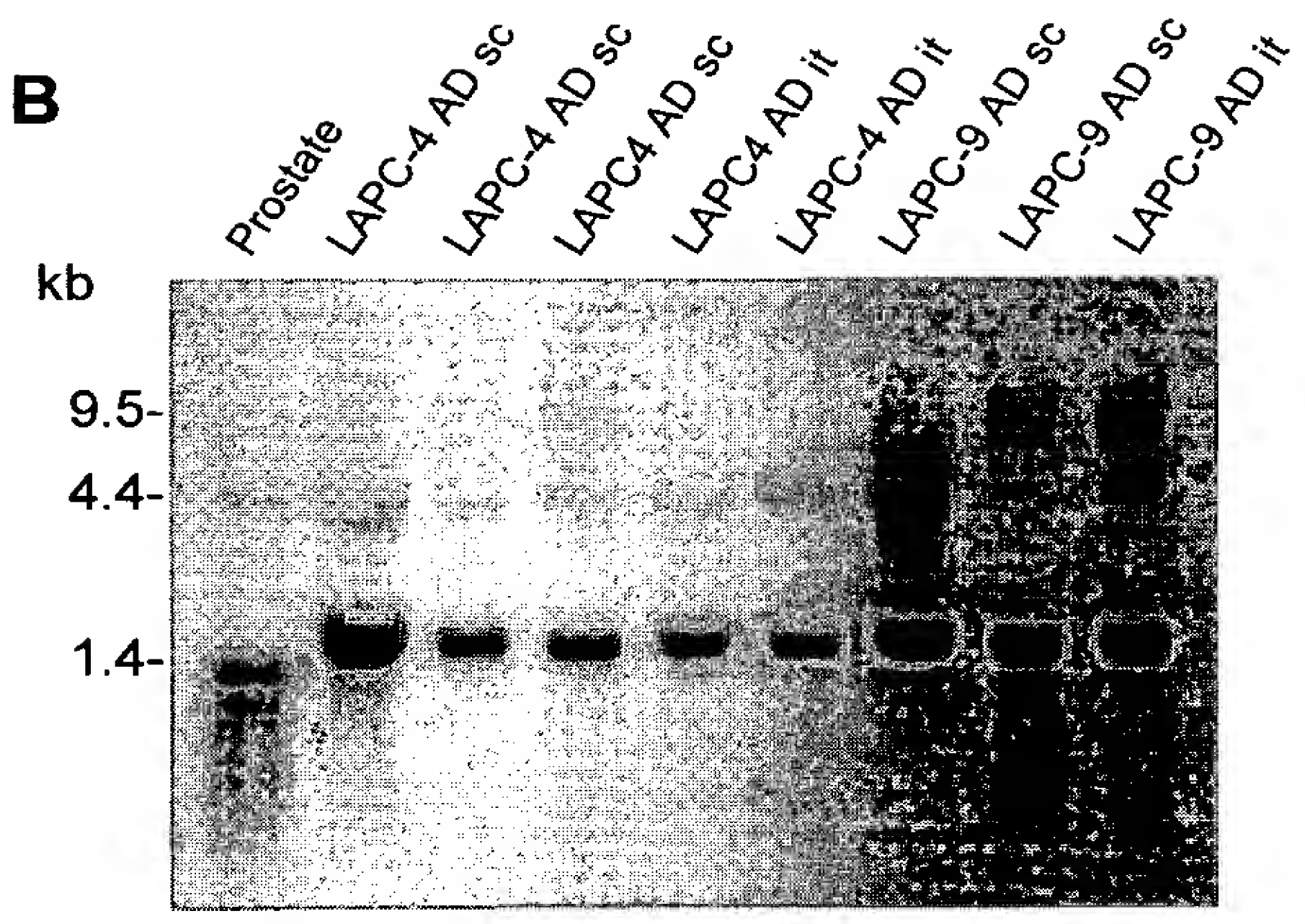
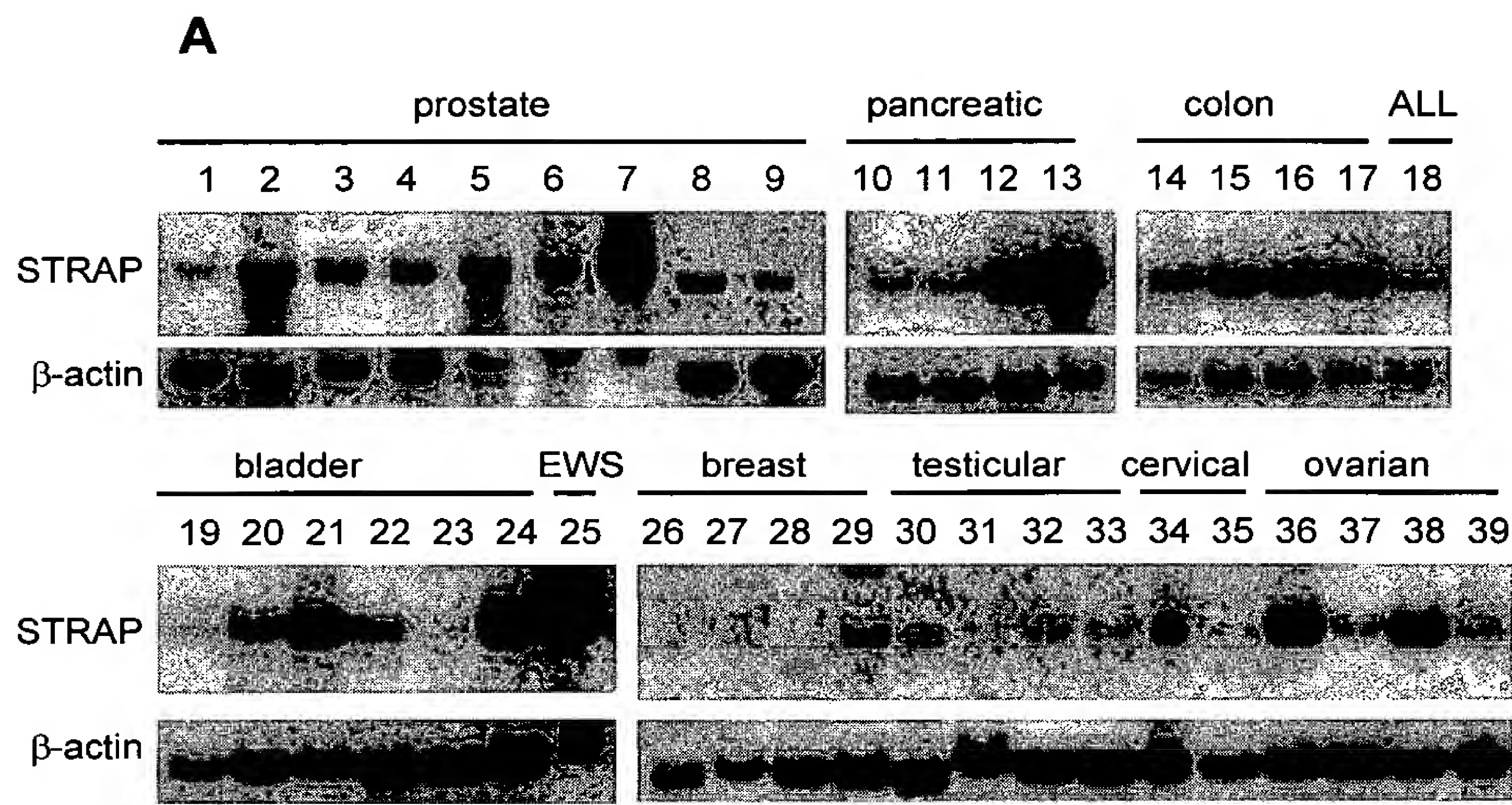


FIG. 6

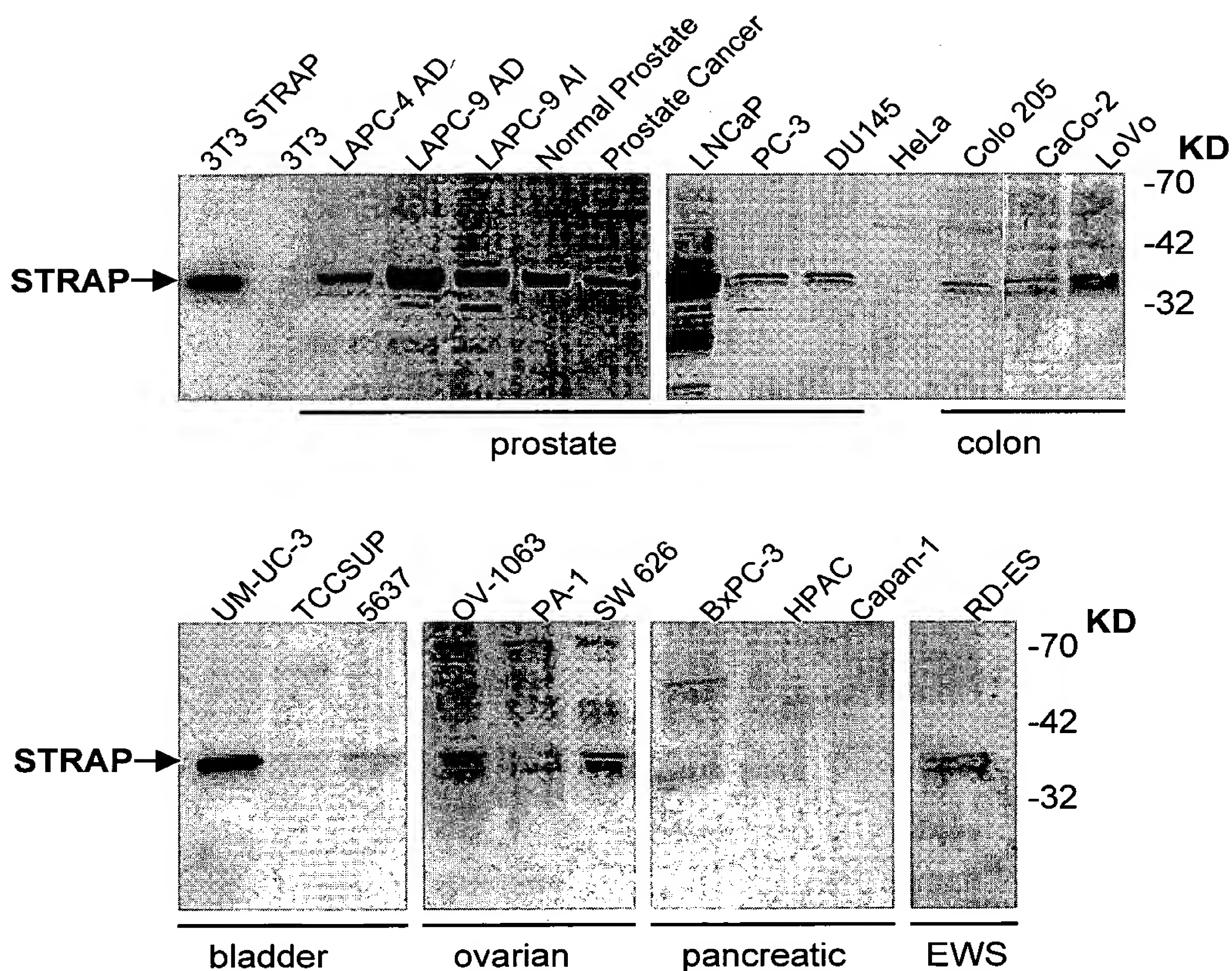
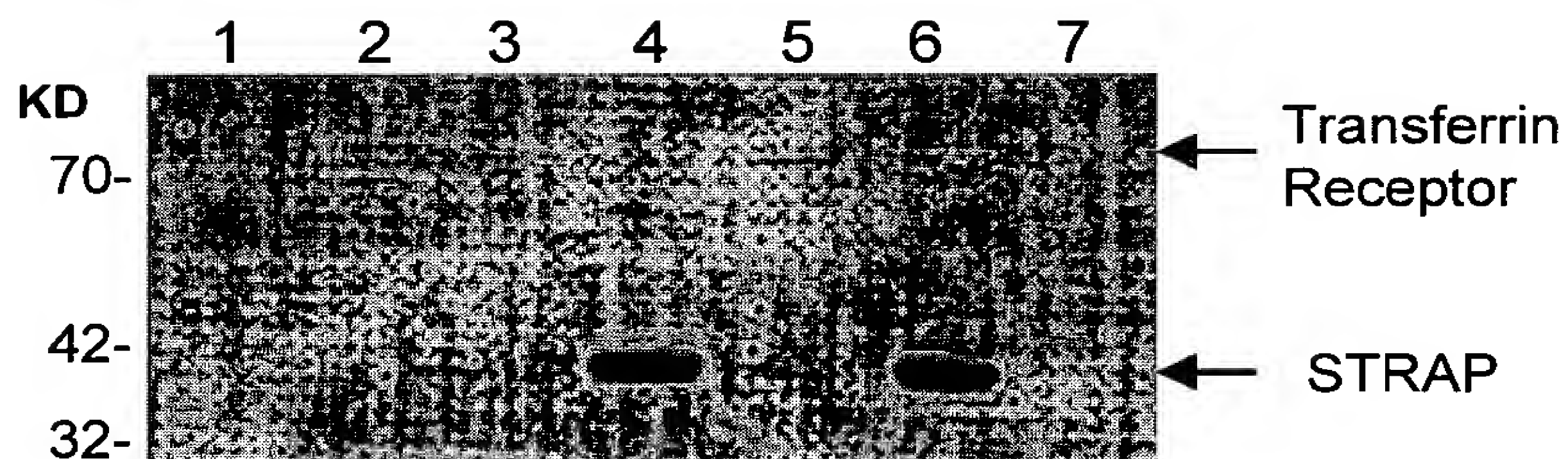


FIG. 7

A



B

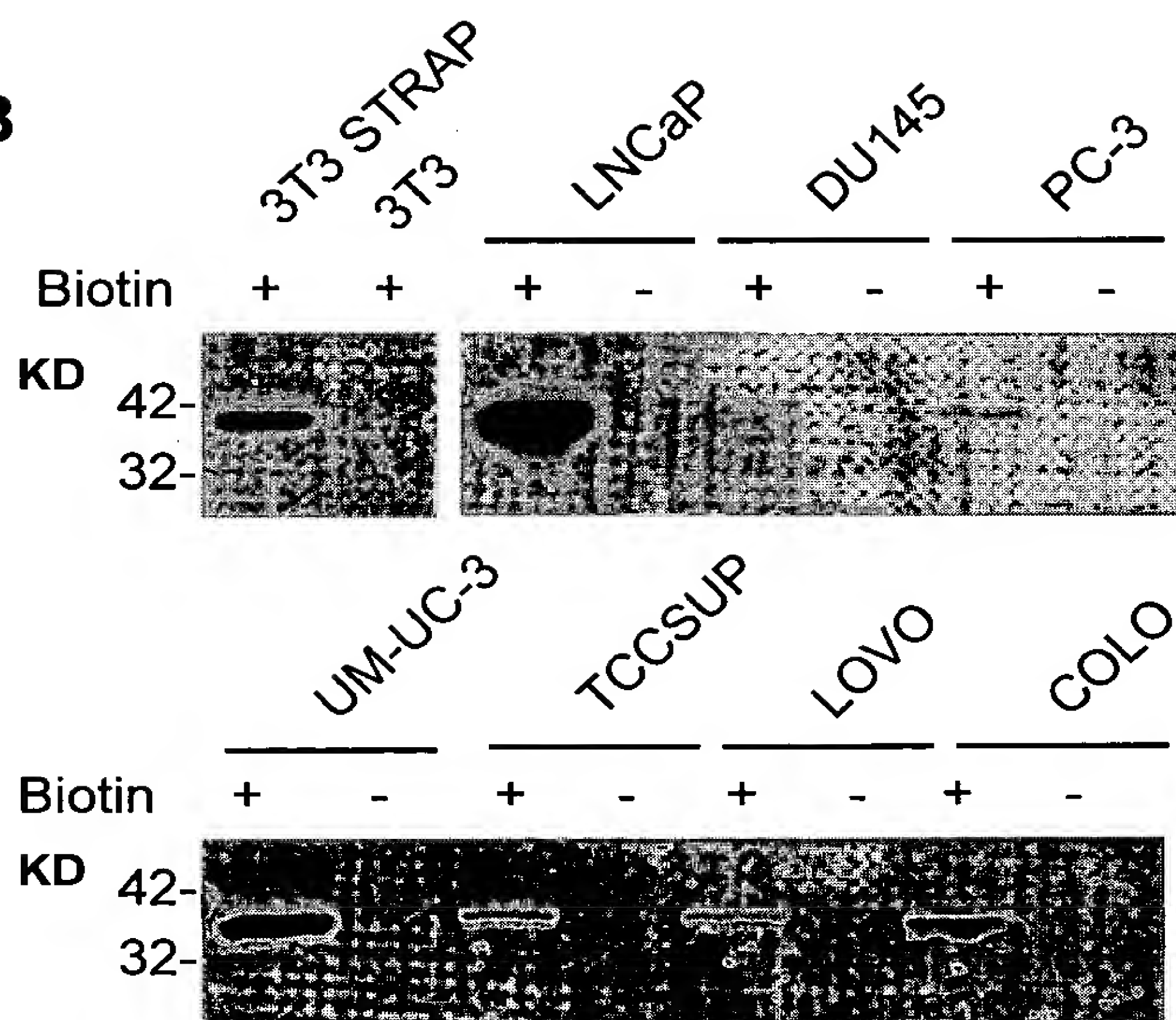


FIG. 8

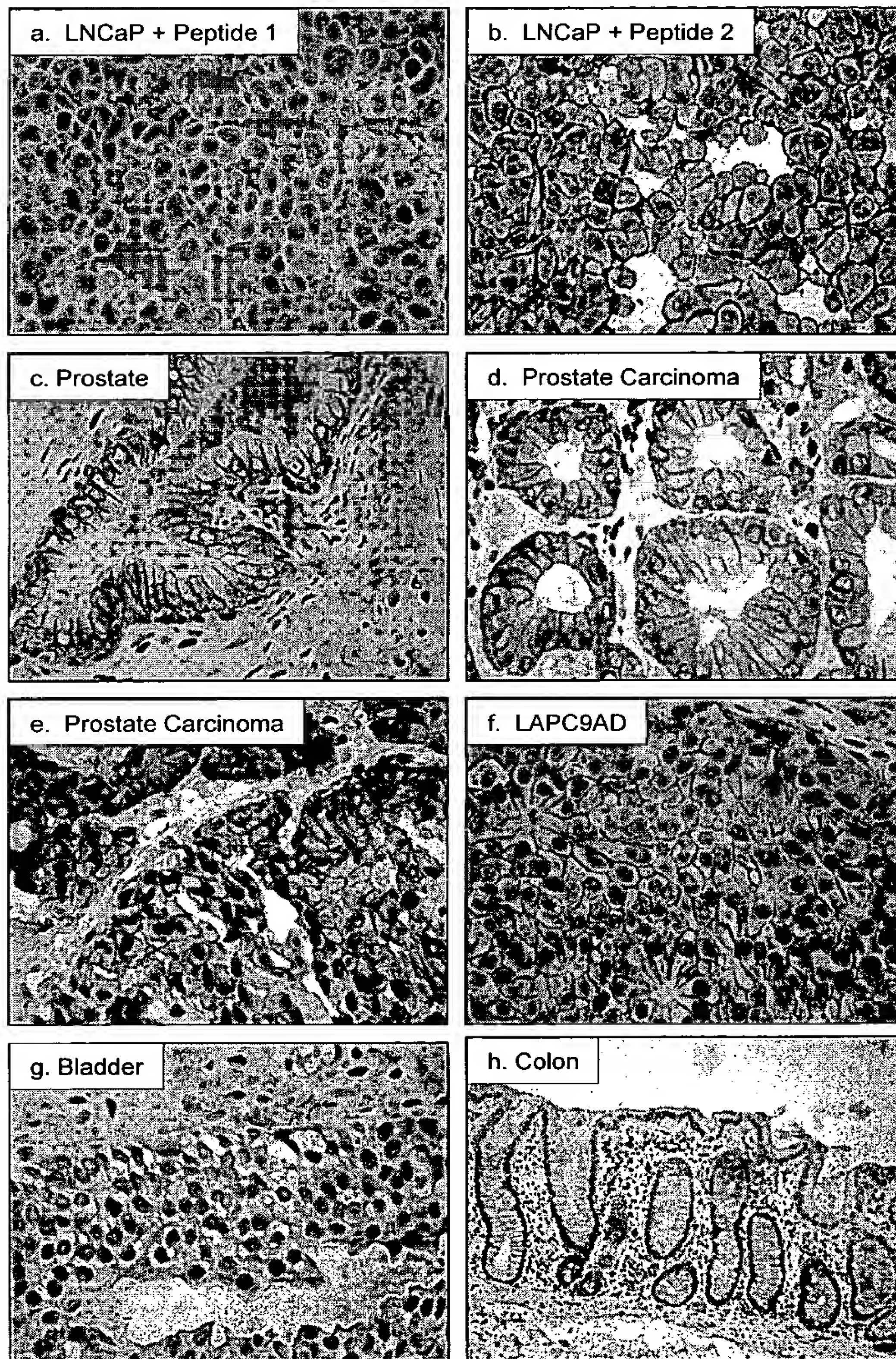


FIG. 9

5'			10			19			28			37			46			55		
	GGA	CGC	GTG	GGC	GGA	CGC	GTG	GGT	TCC	TCG	GGC	CCT	CGG	CGC	CAC	AAG	CTG	TCC		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			64			73			82			91			100			109		
	GGG	CAC	GCA	GCC	CCT	AGC	GGC	GCG	TCG	CTG	CCA	AGC	CGG	CCT	CCG	CGC	GCC	TCC		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			118			127			136			145			154			163		
	CTC	CTT	CCT	TCT	CCC	CTG	GCT	GTT	CGC	GAT	CCA	GCT	TGG	GTA	GGC	GGG	GAA	GCA		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			172			181			190			199			208			217		
	GCT	GGA	GTG	CGA	CCG	CCA	CGG	CAG	CCA	CCC	TGC	AAC	CGC	CAG	TCG	GAG	GTG	CAG		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			226			235			244			253			262			271		
	TCC	GTA	GGC	CCT	GGC	CCC	CGG	GTG	GGC	CCT	TGG	GGA	GTC	GGC	GCC	GCT	CCC	GAG		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			280			289			298			307			316			325		
	GAG	CTG	CAA	GGC	TCG	CCC	CTG	CCC	GGC	GTG	GAG	GGC	GCG	GGG	GGC	GCG	GAG	GAT		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			334			343			352			361			370			379		
	ATT	CTT	GGT	GAT	CTT	GGA	AGT	GTC	CGT	ATC	ATG	GAA	TCA	ATC	TCT	ATG	ATG	GGA		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
													M	E	S	I	S	M	M	G
			388			397			406			415			424			433		
	AGC	CCT	AAG	AGC	CTT	AGT	GAA	ACT	TGT	TTA	CCT	AAT	GGC	ATA	AAT	GGT	ATC	AAA		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	S	P	K	S	L	S	E	T	C	L	P	N	G	I	N	G	I	K		
			442			451			460			469			478			487		
	GAT	GCA	AGG	AAG	GTC	ACT	GTA	GGT	GTG	ATT	GGA	AGT	GGA	GAT	TTT	GCC	AAA	TCC		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	D	A	R	K	V	T	V	G	V	I	G	S	G	D	F	A	K	S		
			496			505			514			523			532			541		
	TTG	ACC	ATT	CGA	CTT	ATT	AGA	TGC	GGC	TAT	CAT	GTG	GTC	ATA	GGA	AGT	AGA	AAT		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	L	T	I	R	L	I	R	C	G	Y	H	V	V	I	G	S	R	N		
			550			559			568			577			586			595		
	CCT	AAG	TTT	GCT	TCT	GAA	TTT	TTT	CCT	CAT	GTG	GTA	GAT	GTC	ACT	CAT	CAT	GAA		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	P	K	F	A	S	E	F	F	P	H	V	V	D	V	T	H	H	E		
			604			613			622			631			640			649		
	GAT	GCT	CTC	ACA	AAA	ACA	AAT	ATA	ATA	TTT	GTT	GCT	ATA	CAC	AGA	GAA	CAT	TAT		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	D	A	L	T	K	T	N	I	I	F	V	A	I	H	R	E	H	Y		
			658			667			676			685			694			703		
	ACC	TCC	CTG	TGG	GAC	CTG	AGA	CAT	CTG	CTT	GTG	GGT	AAA	ATC	CTG	ATT	GAT	GTG		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	T	S	L	W	D	L	R	H	L	L	V	G	K	I	L	I	D	V		
			712			721			730			739			748			757		
	AGC	AAT	AAC	ATG	AGG	ATA	AAC	CAG	TAC	CCA	GAA	TCC	AAT	GCT	GAA	TAT	TTG	GCT		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	S	N	N	M	R	I	N	Q	Y	P	E	S	N	A	E	Y	L	A		

766	775	784	793	802	811
TCA TTA TTC CCA GAT	TCT TTG ATT GTC	AAA GGA TTT AAT	GTT GTC TCA GCT	TGG	
---	---	---	---	---	
S L F P D	S L I V K G	F N V V	S A W		
820	829	838	847	856	865
GCA CTT CAG TTA GGA	CCT AAG GAT GCC	AGC CGG CAG GTT	TAT ATA TGC	AGC AAC	
---	---	---	---	---	
A L Q L G	P K D A S R	Q V Y I C	S N		
874	883	892	901	910	919
AAT ATT CAA GCG CGA	CAA CAG GTT ATT	GAA CTT GCC CGC	CAG TTG AAT TTC	ATT	
---	---	---	---	---	
N I Q A R	Q Q V I E L	A R Q L N	F I		
928	937	946	955	964	973
CCC ATT GAC TTG GGA	TCC TTA TCA TCA	GCC AGA GAG ATT	GAA AAT TTA CCC	CTA	
---	---	---	---	---	
P I D L G	S L S S A R	E I E N L	P <u>L</u>		
982	991	1000	1009	1018	1027
CGA CTC TTT ACT CTC	TGG AGA GGG CCA	GTG GTG GTA GCT	ATA AGC TTG GCC	ACA	
---	---	---	---	---	
<u>R L F T L W R G P V V V A I S L A T</u>					
1036	1045	1054	1063	1072	1081
TTT TTT TTC CTT TAT	TCC TTT GTC AGA	GAT GTG ATT CAT	CCA TAT GCT AGA	AAC	
---	---	---	---	---	
<u>F F F L</u> Y S F V R D V I H P Y A R N					
1090	1099	1108	1117	1126	1135
CAA CAG AGT GAC TTT	TAC AAA ATT CCT	ATA GAG ATT GTG	AAT AAA ACC TTA	CCT	
---	---	---	---	---	
Q Q S D F Y K I P I E I	<u>V N K T L P</u>				
1144	1153	1162	1171	1180	1189
ATA GTT GCC ATT ACT	TTG CTC TCC CTA	GTA TAC CTT GCA	GGT CTT CTG GCA	GCT	
---	---	---	---	---	
<u>I V A I T L L S L V Y L A G L L A A</u>					
1198	1207	1216	1225	1234	1243
GCT TAT CAA CTT TAT	TAC GGC ACC AAG	TAT AGG AGA TTT	CCA CCT TGG TTG	GAA	
---	---	---	---	---	
A Y Q L Y Y G T K Y R R F P P W L E					
1252	1261	1270	1279	1288	1297
ACC TGG TTA CAG TGT	AGA AAA CAG CTT	GGA TTA CTA AGT	TTT TTC TTC GCT	ATG	
---	---	---	---	---	
T W L Q C R K <u>Q L G L L S F F F A M</u>					
1306	1315	1324	1333	1342	1351
GTC CAT GTT GCC TAC	AGC CTC TGC TTA	CCG ATG AGA AGG	TCA GAG AGA TAT	TTG	
---	---	---	---	---	
<u>V H V A Y S L C L P M</u> R R S E R Y L					
1360	1369	1378	1387	1396	1405
TTT CTC AAC ATG GCT	TAT CAG CAG GTT	CAT GCA AAT ATT	GAA AAC TCT TGG	AAT	
---	---	---	---	---	
F L N M A Y Q Q V H A N I E N S W N					
1414	1423	1432	1441	1450	1459
GAG GAA GAA GTT TGG	AGA ATT GAA ATG	TAT ATC TCC TTT	GGC ATA ATG AGC	CTT	
---	---	---	---	---	
E E E V W R I E <u>M Y I S F G I M S L</u>					

1468	1477	1486	1495	1504	1513
GGC TTA CTT TCC CTC CTG	GCA GTC ACT TCT ATC CCT TCA	GTG AGC AAT GCT TTA			
<u>G L L S L L</u>	<u>A V T S I P S</u>	<u>V S N A L</u>			
1522	1531	1540	1549	1558	1567
AAC TGG AGA GAA TTC AGT	TTT ATT CAG TCT ACA CTT GGA	TAT GTC GCT CTG CTC			
<u>N W R E F S</u>	<u>F I Q S T L G Y V A L L</u>				
1576	1585	1594	1603	1612	1621
ATA AGT ACT TTC CAT GTT	TTA ATT TAT GGA TGG AAA	CGA GCT TTT GAG GAA GAG			
<u>I S T F H V L I Y G W</u>	<u>K R A F E E E</u>				
1630	1639	1648	1657	1666	1675
TAC TAC AGA TTT TAT ACA	CCA CCA AAC TTT GTT CTT	GCT CTT GTT TTG CCC TCA			
<u>Y Y R F Y T P P N F V L A L V L P S</u>					
1684	1693	1702	1711	1720	1729
ATT GTA ATT CTG GAT CTT	TTG CAG CTT TGC AGA TAC	CCA GAC TGA GCT GGA ACT			
<u>I V I L D L L Q L C</u>	<u>R Y P D *</u>				
1738	1747	1756	1765	1774	1783
GGA ATT TGT CTT CCT ATT	GAC TCT ACT TCT TTA AAA	GCG GCT GCC CAT TAC ATT			
1792	1801	1810	1819	1828	1837
CCT CAG CTG TCC TTG CAG	TTA GGT GTA CAT GTG ACT	GAG TGT TGG CCA GTG AGA			
1846	1855	1864	1873	1882	1891
TGA AGT CTC CTC AAA GGA	AGG CAG CAT GTG TCC TTT	TTC ATC CCT TCA TCT TGC			
1900	1909	1918	1927	1936	1945
TGC TGG GAT TGT GGA TAT	AAC AGG AGC CCT GGC AGC	TGT CTC CAG AGG ATC AAA			
1954	1963	1972	1981	1990	1999
GCC ACA CCC AAA GAG TAA	GGC AGA TTA GAG ACC AGA	AAG ACC TTG ACT ACT TCC			
2008	2017	2026	2035	2044	2053
CTA CTT CCA CTG CTT TTC	CTG CAT TTA AGC CAT TGT	AAA TCT GGG TGT GTT ACA			
2062	2071	2080	2089	2098	2107
TGA AGT GAA AAT TAA TTC	TTT CTG CCC TTC AGT TCT	TTA TCC TGA TAC CAT TTA			
2116	2125	2134	2143	2152	2161
ACA CTG TCT GAA TTA ACT	AGA CTG CAA TAA TTC TTT	CTT TTG AAA GCT TTT AAA			
2170	2179	2188	2197	2206	2215
GGA TAA TGT GCA ATT CAC	ATT AAA ATT GAT TTT CCA	TTG TCA ATT AGT TAT ACT			
2224	2233	2242	2251	2260	2269
CAT TTT CCT GCC TTG ATC	TTT CAT TAG ATA TTT TGT	ATC TGC TTG GAA TAT ATT			
2278	2287	2296	2305	2314	2323
ATC TTC TTT TTA ACT GTG	TAA TTG GTA ATT ACT AAA	ACT CTG TAA TCT CCA AAA			
2332	2341	2350	2359	2368	2377
TAT TGC TAT CAA ATT ACA	CAC CAT GTT TTC TAT CAT	TCT CAT AGA TCT GCC TTA			
2386	2395	2404	2413	2422	2431
TAA ACA TTT AAA TAA AAA	GTA CTA TTT AAT GAT TTA	AAA AAA AAA AAA AAA AAA			
2440	2449				
AAA AAA AAA AAA AAA AAA	AAA AA 3'				

FIG. 10A

1 CGAAACTTCC CTCTACCCGC CCGGCCCGCG GCGCGCACCG TTGGCGCTGG ACGCTTCCTC
 GCTTTGAAGG GAGATGGGCG GGCCGGGCGC CGCGCGTGGC AACCGCGACC TGCGAAGGAG

61 CTTGGAAGCG CCTCTCCCTC **AGTTATGGAG** M E K T C I D A L P L T
 AAAACTTGTA TAGATGCACT TCCTCTTACT
 GAACCTTCGC GGAGAGGGAG TCAATACCTC TTTTGAACAT ATCTACGTGA AGGAGAATGA

121 M N S S E K Q E T V C I F G T G D F G R
 ATGAATTCTT CAGAAAAGCA AGAGACTGTA TGTATTTTGT GAACTGGTGA TTTTGGGAAGA
 TACTTAAGAA GTCTTTTCGT TCTCTGACAT ACATAAAAAC CTTGACCACT AAAACCTTCT

181 S L G L K M L Q C G Y S V V F G S R N P
 TCACTGGGAT TGAAAATGCT CCAGTGTGGT TATTCTGTTG TTTTGGGAAG TCGAAACCCC
 AGTGACCCTA ACTTTTACGA GGTCACACCA ATAAGACAAC AAAAACCTTC AGCTTTGGGG

241 Q K T T L L P S G A E V L S Y S E A A K
 CAGAAGACCA CCCTACTGCC CAGTGGTGCA GAAGTCTTGA GCTATTCAGA AGCAGCCAAG
 GTCTTCTGGT GGGATGACGG GTCACCACGT CTTCAGAACT CGATAAGTCT TCGTCGGTTC

301 K S G I I I I A I H R E H Y D F L T E L
 AAGTCTGGCA TCATAATCAT AGCAATCCAC AGAGAGCATT ATGATTTTCT CACAGAATTA
 TTCAGACCGT AGTATTAGTA TCGTTAGGTG TCTCTCGTAA TACTAAAAGA GTGTCTTAAT

361 T E V L N G K I L V D I S N N L K I N Q
 ACTGAGGTTC TCAATGGAAA AATATTGGTA GACATCAGCA ACAACCTCAA AATCAATCAA
 TGACTCCAAG AGTTACCTTT TTATAACCAT CTGTAGTCGT TGTGAGGTT TTAGTTAGTT

421 Y P E S N A E Y L A H L V P G A H V V K
 TATCCAGAAT CTAATGCAGA GTACCTTGCT CATTTGGTGC CAGGAGCCCA CGTGGTAAAA
 ATAGGTCTTA GATTACGTCT CATGGAACGA GTAAACCACG GTCCTCGGGT GCACCATTTT

481 A F N T I S A W A L Q S G A L D A S R Q
 GCATTTAACA CCATCTCAGC CTGGGCTCTC CAGTCAGGAG CACTGGATGC AAGTCGGCAG
 CGTAAATTGT GGTAGAGTCG GACCCGAGAG GTCAGTCCTC GTGACCTACG TTCAGCCGTC

541 V F V C G N D S K A K Q R V M D I V R N
 GTGTTTGTGT GTGGAAATGA CAGCAAAGCC AAGCAAAGAG TGATGGATAT TGTTTCGTAAT
 CACAAACACA CACCTTTACT GTCGTTTCGG TTCGTTTCTC ACTACCTATA ACAAGCATTA

601 L G L T P M D Q G S L M A A K E I E K Y
 CTTGGACTTA CTCCAATGGA TCAAGGATCA CTCATGGCAG CCAAAGAAAT TGAAAAGTAC
 GAACCTGAAT GAGGTTACCT AGTTCCTAGT GAGTACCGTC GGTTTCTTTA ACTTTTCATG

661 P L Q L F P M W R F P F Y L S A V L C V
 CCCCTGCAGC TATTTCCAAT GTGGAGGTTT CCCTTCTATT TGTCTGCTGT GCTGTGTGTC
 GGGGACGTCG ATAAAGGTTA CACCTCCAAG GGAAGATAA ACAGACGACA CGACACACAG

721 F L F F Y C V I R D V I Y P Y V Y E K K
 TTCTTGTTTT TCTATTGTGT TATAAGAGAC GTAATCTACC CTTATGTTTA TGAAAAGAAA
 AAGAACAAAA AGATAACACA ATATTCTCTG CATTAGATGG GAATACAAAT ACTTTTCTTT

781 D N T F R M A I S I P N R I F P I T A L
 GATAATACAT TTCGTATGGC TATTTCCATT CCAAATCGTA TCTTTCCAAT AACAGCACTT
 CTATTATGTA AAGCATAACCG ATAAAGGTAA GGTTTAGCAT AGAAAGGTAA TTGTCGTGAA

841 T L L A L V Y L P G V I A A I L Q L Y R
 AACTGCTTG CTTTGGTTTA CCTCCCTGGT GTTATTGCTG CCATTCTACA ACTGTACCGA
 TGTGACGAAC GAAACCAAAT GGAGGGACCA CAATAACGAC GGTAAGATGT TGACATGGCT

901 G T K Y R R F P D W L D H W M L C R K Q
 GGCACAAAAT ACCGTCGATT CCCAGACTGG CTTGACCACT GGATGCTTTG CCGAAAGCAG
 CCGTGTTTTA TGGCAGCTAA GGGTCTGACC GAACTGGTGA CCTACGAAAC GGCTTTCGTC

961 L G L V A L G F A F L H V L Y T L V I P
 CTTGGCTTGG TAGCTCTGGG ATTTGCCTTC CTTCATGTCC TCTACACACT TGTGATTCCT
 GAACCGAACC ATCGAGACCC TAAACGGAAG GAAGTACAGG AGATGTGTGA AACTAAGGA

1021 I R Y Y V R W R L G N L T V T Q A I L K
 ATTCGATATT ATGTACGATG GAGATTGGGA AACTTAACCG TTACCCAGGC AATACTCAAG
 TAAGCTATAA TACATGCTAC CTCTAACCTT TTGAATTGGC AATGGGTCCG TTATGAGTTC

1081 K E N P F S T S S A W L S D S Y V A L G
 AAGGAGAATC CATTTAGCAC CTCCTCAGCC TGGCTCAGTG ATTCATATGT GGCTTTGGGA
 TTCCTCTTAG GTAAATCGTG GAGGAGTCGG ACCGAGTCAC TAAGTATACA CCGAAACCCT

1141 I L G F F L F V L L G I T S L P S V S N
 ATACTTGGGT TTTTCTGTGTT TGTACTCTTG GGAATCACTT CTTTGCCATC TGTTAGCAAT
 TATGAACCCA AAAAAGACAA ACATGAGAAC CCTTAGTGAA GAAACGGTAG ACAATCGTTA

1201 A V N W R E F R F V Q S K L G Y L T L I
 GCAGTCAACT GGAGAGAGTT CCGATTTGTC CAGTCCAAAC TGGGTTATTT GACCCTGATC
 CGTCAGTTGA CCTCTCTCAA GGCTAAACAG GTCAGGTTTG ACCCAATAAA CTGGGACTAG

1261 L C T A H T L V Y G G K R F L S P S N L
 TTGTGTACAG CCCACACCCT GGTGTACGGT GGGAAGAGAT TCCTCAGCCC TTCAAATCTC
 AACACATGTC GGGTGTGGGA CCACATGCCA CCCTTCTCTA AGGAGTCGGG AAGTTTAGAG

1321 R W Y L P A A Y V L G L I I P C T V L V
 AGATGGTATC TTCCTGCAGC CTACGTGTTA GGGCTTATCA TTCCTTGCAC TGTGCTGGTG
 TCTACCATAG AAGGACGTCG GATGCACAAT CCCGAATAGT AAGGAACGTG ACACGACCAC

1381 I K F V L I M P C V D N T L T R I R Q G
 ATCAAGTTTG TCCTAATCAT GCCATGTGTA GACAACACCC TTACAAGGAT CCGCCAGGGC
 TAGTTCAAAC AGGATTAGTA CGGTACACAT CTGTTGTGGG AATGTTCTTA GGCGGTCCCG

1441 W E R N S K H
 TGGGAAAGGA ACTCAAAACA CTAGAAAAG CATTGAATGG AAAATCAATA TTTAAAACAA
 ACCCTTTCCT TGAGTTTTGT GATCTTTTTC GTAACCTACC TTTTAGTTAT AAATTTTGTT

1501 AGTTCAATTT AGCTGGATTT CTGAACTATG GTTTTGAATG TTTAAAGAAG AATGATGGGT
 TCAAGTTAAA TCGACCTAAA GACTTGATAC CAAACTTAC AAATTTCTTC TTACTACCCA

1561 ACAGTTAGGA AAGTTTTTTT CTTACACCGT GACTGAGGGA AACATTGCTT GTCTTTGAGA
 TGTCATTCCT TTCAAAAAA GAATGTGGCA CTGACTCCCT TTGTAACGAA CAGAACTCT

1621 AATTGACTGA CATACTGGAA GAGAACACCA TTTTATCTCA GGTTAGTGAA GAATCAGTGC
 TTAAGTACT GTATGACCTT CTCTTGTTGGT AAAATAGAGT CCAATCACTT CTTAGTCACG

1681	AGGTCCCTGA	CTCTTATTTT	CCCAGAGGCC	ATGGAGCTGA	GATTGAGACT	AGCCTTGTGG
	TCCAGGGACT	GAGAATAAAA	GGGTCTCCGG	TACCTCGACT	CTAACTCTGA	TCGGAACACC
1741	TTTCACACTA	AAGAGTTTCC	TTGTTATGGG	CAACATGCAT	GACCTAATGT	CTTGCAAAAT
	AAAGTGTGAT	TTCTCAAAGG	AACAATACCC	GTTGTACGTA	CTGGATTACA	GAACGTTTTA
1801	CCAATAGAAG	TATTGCAGCT	TCCTTCTCTG	GCTCAAGGGC	TGAGTTAAGT	GAAAGGAAAA
	GGTTATCTTC	ATAACGTCGA	AGGAAGAGAC	CGAGTTCCCG	ACTCAATTCA	CTTTCCTTTT
1861	ACAGCACAAT	GGTGACCACT	GATAAAGGCT	TTATTAGGTA	TATCTGAGGA	AGTGGGTCAC
	TGTCGTGTTA	CCACTGGTGA	CTATTTCCGA	AATAATCCAT	ATAGACTCCT	TCACCCAGTG
1921	ATGAAATGTA	AAAAGGGAAT	GAGGTTTTTG	TTGTTTTTTG	GAAGTAAAGG	CAAACATAAA
	TACTTTACAT	TTTTCCCTTA	CTCCAAAAAC	AACAAAAAAC	CTTCATTTCC	GTTTGTATTT
1981	TATTACCATG	ATGAATTCTA	GTGAAATGAC	CCCTTGACTT	TGCTTTTCTT	AATACAGATA
	ATAATGGTAC	TACTTAAGAT	CACTTTACTG	GGGAACTGAA	ACGAAAAGAA	TTATGTCTAT
2041	TTTACTGAGA	GGAACATTTT	TTATAACACA	AGAAAAATTT	ACAATTGATT	AAAAGTATCC
	AAATGACTCT	CCTTGATAAA	AATATTGTGT	TCTTTTTTAA	TGTAACTAA	TTTTCATAGG
2101	ATGTCTTGGA	TACATACGTA	TCTATAGAGC	TGGCATGTAA	TTCTTCCTCT	ATAAAGAATA
	TACAGAACCT	ATGTATGCAT	AGATATCTCG	ACCGTACATT	AAGAAGGAGA	TATTTCTTAT
2161	GGTATAGGAA	AGACTGAATA	AAAATGGAGG	GATATCCCCT	TGGATTTTAC	TTGCATTGTG
	CCATATCCTT	TCTGACTTAT	TTTTACCTCC	CTATAGGGGA	ACCTAAAGTG	AACGTAACAC
2221	CAATAAGCAA	AGAAGGGTTG	ATAAAAGTTC	TTGATCAAAA	AGTTCAAAGA	AACCAGAATT
	GTTATTCGTT	TCTTCCCAAC	TATTTTCAAG	AACTAGTTTT	TCAAGTTTCT	TTGGTCTTAA
2281	TTAGACAGCA	AGCTAAATAA	ATATTGTAAA	ATTGCACTAT	ATTAGGTTAA	GTATTATTTA
	AATCTGTCGT	TCGATTTATT	TATAACATTT	TAACGTGATA	TAATCCAATT	CATAATAAAT
2341	GGTATTATAA	TATGCTTTGT	AAATTTTATA	TTCCAAATAT	TGCTCAATAT	TTTTCATCTA
	CCATAATATT	ATACGAAACA	TTTAAAATAT	AAGGTTTATA	ACGAGTTATA	AAAAGTAGAT
2401	TTAAATTAAT	TTCTAGTGTA	AATAAGTAGC	TTCTATATCT	GTCTTAGTCT	ATTATAATTG
	AATTTAATTA	AAGATCACAT	TTATTCATCG	AAGATATAGA	CAGAATCAGA	TAATATTAAC
2461	TAAGGAGTAA	AATTAAATGA	ATAGTCTGCA	GGTATAAATT	TGAACAATGC	ATAGATGATC
	ATTCCTCATT	TTAATTTACT	TATCAGACGT	CCATATTTAA	ACTTGTTACG	TATCTACTAG
2521	GAAAATTACG	GAAAATCATA	GGGCAGAGAG	GTGTGAAGAT	TCATCATTAT	GTGAAATTTG
	CTTTTAATGC	CTTTTAGTAT	CCCGTCTCTC	CACACTTCTA	AGTAGTAATA	CACTTTAAAC
2581	GATCTTTCTC	AAATCCTTGC	TGAAATTTAG	GATGGTTCTC	ACTGTTTTTC	TGTGCTGATA
	CTAGAAAGAG	TTTAGGAACG	ACTTTAAATC	CTACCAAGAG	TGACAAAAAG	ACACGACTAT
2641	GTACCCTTTC	CAAGGTGACC	TTCAGGGGGA	TTAACCTTCC	TAGCTCAAGC	AATGAGCTAA
	CATGGGAAAG	GTTCCACTGG	AAGTCCCCCT	AATTGGAAGG	ATCGAGTTCC	TTACTCGATT
2701	AAGGAGCCTT	ATGCATGATC	TTCCCACATA	TCAAAATAAC	TAAAAGGCAC	TGAGTTTGGC
	TTCTCGGAA	TACGTACTAG	AAGGGTGTAT	AGTTTTATTG	ATTTTCCGTG	ACTCAAACCG
2761	ATTTTTCTGC	CTGCTCTGCT	AAGACCTTTT	TTTTTTTTTT	ACTTTCATTA	TAACATATTA
	TAAAAAGACG	GACGAGACGA	TTCTGGAAAA	AAAAAAAAAA	TGAAAGTAAT	ATTGTATAAT

2821	TACATGACAT	TATACAAAAA	TGATTAAAAT	ATATTAAAAC	AACATCAACA	ATCCAGGATA
	ATGTACTGTA	ATATGTTTTT	ACTAATTTTA	TATAATTTTG	TTGTAGTTGT	TAGGTCCTAT
2881	TTTTTCTATA	AAACTTTTTA	AAAATAATTG	TATCTATATA	TTCAATTTTA	CATCCTTTTT
	AAAAAGATAT	TTTGAAAAAT	TTTTATTAAC	ATAGATATAT	AAGTTAAAAT	GTAGGAAAAA
2941	CAAAGGCTTT	GTTTTTCTAA	AGGCTTTGTT	TTCCTTTTTA	TTATTTTTTT	CTTTTTTATT
	GTTTCCGAAA	CAAAAAGATT	TCCGAAACAA	AAGGAAAAAT	AATAAAAAAA	GAAAAAATAA
3001	TTTTTGAGAC	AGTCTTGCTC	TGTCGCTCAG	GCTGGAGTGC	AGTGGCACGA	TCTCAGCTCA
	AAAAACTCTG	TCAGAACGAG	ACAGCGAGTC	CGACCTCACG	TCACCGTGCT	AGAGTCGAGT
3061	CTGCAACCTC	CTCCTCCCAG	GTTCAAGTGA	TTCTTGTTCA	TCAGCCTCCC	GAGTAGCTGG
	GACGTTGGAG	GAGGAGGGTC	CAAGTTCACT	AAGAACAAGT	AGTCGGAGGG	CTCATCGACC
3121	GACTACAGGC	ATGTGCCACT	ATGCCCAGCT	AATTTTTGTA	CTTTTAGTAG	AGACAGGGTT
	CTGATGTCCG	TACACGGTGA	TACGGGTCGA	TTAAAAACAT	GAAAATCATC	TCTGTCCCAA
3181	TCACCACATT	GGTCAGGCTG	GTCTTGAAAT	GCTGGCGTCA	AGTGATCTGC	CTGCCTCCGC
	AGTGGTGTA	CCAGTCCGAC	CAGAACTTTA	CGACCGCAGT	TCACTAGACG	GACGGAGGCG
3241	CTTACGTAAT	ATATTTTCTT	AATGGCTGCA	TAATATCACA	TCAAATAGGC	ATTTTTCAAA
	GAATGCATTA	TATAAAAGAA	TTACCGACGT	ATTATAGTGT	AGTTTATCCG	TAAAAAGTTT
3301	CCTCTTTCCT	TATTAAACAT	GTAGACTATA	TCCATTTTTT	ACTAAAATAA	ATAACATTTC
	GGAGAAAGGA	ATAATTTGTA	CATCTGATAT	AGGTAAAAAA	TGATTTTATT	TATTGTAAAG
3361	AGATAATATC	TTTGCACTGA	TAATGTTGCC	AAGCCATTTC	TAAAGTGACC	TTATCAATTT
	TCTATTATAG	AAACGTGACT	ATTACAACGG	TTCGGTAAAG	ATTCTACTGG	AATAGTTAAA
3421	AATTACCATT	GGATGAGGGT	GTTGCTTTCA	TCGCACCATT	GTAGATTGTC	TTTTTTATTT
	TTAATGGTAA	CCTACTCCCA	CAACGAAAGT	AGCGTGGTAA	CATCTAACAG	AAAAAATAAA
3481	CAATTTGCGT	TTATTTATAA	CTGGTTGCAA	AGGTACACAG	AACACACGCT	CCTTCAACTT
	GTAAACGCA	AATAAATATT	GACCAACGTT	TCCATGTGTC	TTGTGTGCGA	GGAAGTTGAA
3541	ATCTTTGATA	AACCCAAGCA	AGGATACAAA	AAGTTGGACG	ACATTGAGTA	GAGTCATGGT
	TAGAAACTAT	TTGGGTTTCG	TCCTATGTTT	TTCAACCTGC	TGTAACCTCAT	CTCAGTACCA
3601	ATACGGTGCT	GACCCTACAG	TATCAGTGGA	AAAGATAAGG	AAAATGTCAC	TACTCACCTA
	TATGCCACGA	CTGGGATGTC	ATAGTCACCT	TTTCTATTCC	TTTTACAGTG	ATGAGTGGAT
3661	TGTTATGCAA	AACAGTTAGG	TGTGCTGGGG	CTGGATACTG	CTCTTTTACT	TGAGCATTGG
	ACAATACGTT	TTGTCAATCC	ACACGACCCC	GACCTATGAC	GAGAAAATGA	ACTCGTAACC
3721	TTGATTAAAG	TTTAGGTACC	ATCCAGGCTG	GTCTAGAGAA	GTCTTTGGAG	TTAACCATGC
	AACTAATTTT	AAATCCATGG	TAGGTCCGAC	CAGATCTCTT	CAGAAACCTC	AATTGGTACG
3781	TCTTTTTGTT	AAAGAAGAGA	GTAATGTGTT	TATCCTGGCT	CATAGTCCGT	CACCGAAAAT
	AGAAAAACAA	TTTCTTCTCT	CATTACACAA	ATAGGACCGA	GTATCAGGCA	GTGGCTTTTA
3841	AGAAAATGCC	ATCCATAGGT	AAAATGCTGA	CCTATAGAAA	AAAATGAACT	CTACTTTTAT
	TCTTTTACGG	TAGGTATCCA	TTTTACGACT	GGATATCTTT	TTTTACTTGA	GATGAAAATA
3901	AGCCTAGTAA	AAATGCTCTA	CCTGAGTAGT	TAAAAGCAAT	TCATGAAGCC	TGAAGCTAAA
	TCGGATCATT	TTTACGAGAT	GGACTCATCA	ATTTTCGTTA	AGTACTTCGG	ACTTCGATTT

3961 GAGCACTCTG ATGGTTTTGG CATAATAGCT GCATTTCCAG ACCTGACCTT TGGCCCCAAC
CTCGTGAGAC TACCAAAACC GTATTATCGA CGTAAAGGTC TGGACTGGAA ACCGGGGTTG

4021 CACAAGTGCT CCAAGCCCCA CCAGCTGACC AAAGAAAGCC CAAGTTCTCC TTCTGTCCTT
GTGTTACGA GGTTCGGGGT GGTCTGACTGG TTTCTTTTCGG GTTCAAGAGG AAGACAGGAA

4081 CCCACAACCT CCCTGCTCCC AAAACTATGA AATTAATTTG ACCATATTAA CACAGCTGAC
GGGTGTTGGA GGGACGAGGG TTTTGATACT TTAATTAAAC TGGTATAATT GTGTCGACTG

4141 TCCTCCAGTT TACTTAAGGT AGAAAGAATG AGTTTACAAC AGATGAAAAT AAGTGCTTTG
AGGAGGTCAA ATGAATTCCA TCTTTCTTAC TCAAATGTTG TCTACTTTTA TTCACGAAAC

4201 GGCGAACTGT ATTCCTTTTA ACAGATCCAA ACTATTTTAC ATTTAAAAAA AAAGTTAAAC
CCGCTTGACA TAAGGAAAAT TGTCTAGGTT TGATAAAATG TAAATTTTTT TTTCAATTTG

4261 TAAACTTCTT TACTGCTGAT ATGTTTCCTG TATTCTAGAA AAATTTTAC ACTTTCACAT
ATTTGAAGAA ATGACGACTA TACAAAGGAC ATAAGATCTT TTTAAAAATG TGAAAGTGTA

4321 TATTTTTGTA CACTTTCCCC ATGTTAAGGG ATGATGGCTT TTATAAATGT GTATTCATTA
ATAAAAACAT GTGAAAGGGG TACAATTCCC TACTACCGAA AATATTTACA CATAAGTAAT

4381 AATGTTACTT TAAAAATAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
TTACAATGAA ATTTTTATTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

FIG. 10B

STEAP-2, AA508880 (NCI_CGAP Pr6)

ggtcgacttttccctttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgactttttaca
aaattcctatagagattgtgaataaaaaccttacctatagttgccattactttgctctccctagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggttggaacctgggta
cagtgtagaaaacagcttggattactaagttgtttcttcgctatgggtccatggtgcctacagcctctgcttaccga
tgagaagggtcagagagat

STEAP-2, 98P4B6 SSH fragment

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAAGTGGAAATTTGTCTTCCTATTGACTCTACTTCTTTAAAAGCG
GCTGCCCATTACATTTCCTCAGCTGTCCTTGACAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT

STEAP-3, AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctgggtcagtgattcatatgtggctttgggaataacttgggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt
ccagtcctaaactgggttatttgacctgatcttgtgtacagcccacacctgggtgtacgggtgggaagagattcctc
agcccttcaaactctcagatgggtatcttctcctgcagcctacgtgttagggcttatcattccttgcactgtgctgggta
tcaagtttgtcctaatacatgccatgtgttagacaacaccttacaaggatccgccagggtgggaagggaactcaa
acactagaaaaagcattgaatggaaaatcaatatatttaaaacaaagttcaatttagctggaaaaaaaa

STEAP 4, R80991 (placental EST)

ggccgcggcanccgctacgacctgggtcaacctggcagtcagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggttgagatctacctctccctgggagtgctggccctcggcacggtgtccctgctggccg
tgacctcactgccgtccattgcaaactcgctcaactggaggaggttcagcttcgttcagtcctcactgggctttgt
ggcctcgtgctgagcacactncacacgctcacctacggctggaccgcgccttcgaggagagccgctacaagttc
tacctncctccaccttcaagntcacgctgctgggtgcctgcgttcgttcctcctgggccaaagccctgttntac
tgcttgcattcagccgnaga

1911 1899 1897 1895 1893 1891 1889 1887 1885 1883 1881 1879 1877 1875 1873 1871 1869 1867 1865 1863 1861 1859 1857 1855 1853 1851 1849 1847 1845 1843 1841 1839 1837 1835 1833 1831 1829 1827 1825 1823 1821 1819 1817 1815 1813 1811 1809 1807 1805 1803 1801 1799 1797 1795 1793 1791 1789 1787 1785 1783 1781 1779 1777 1775 1773 1771 1769 1767 1765 1763 1761 1759 1757 1755 1753 1751 1749 1747 1745 1743 1741 1739 1737 1735 1733 1731 1729 1727 1725 1723 1721 1719 1717 1715 1713 1711 1709 1707 1705 1703 1701 1699 1697 1695 1693 1691 1689 1687 1685 1683 1681 1679 1677 1675 1673 1671 1669 1667 1665 1663 1661 1659 1657 1655 1653 1651 1649 1647 1645 1643 1641 1639 1637 1635 1633 1631 1629 1627 1625 1623 1621 1619 1617 1615 1613 1611 1609 1607 1605 1603 1601 1599 1597 1595 1593 1591 1589 1587 1585 1583 1581 1579 1577 1575 1573 1571 1569 1567 1565 1563 1561 1559 1557 1555 1553 1551 1549 1547 1545 1543 1541 1539 1537 1535 1533 1531 1529 1527 1525 1523 1521 1519 1517 1515 1513 1511 1509 1507 1505 1503 1501 1499 1497 1495 1493 1491 1489 1487 1485 1483 1481 1479 1477 1475 1473 1471 1469 1467 1465 1463 1461 1459 1457 1455 1453 1451 1449 1447 1445 1443 1441 1439 1437 1435 1433 1431 1429 1427 1425 1423 1421 1419 1417 1415 1413 1411 1409 1407 1405 1403 1401 1399 1397 1395 1393 1391 1389 1387 1385 1383 1381 1379 1377 1375 1373 1371 1369 1367 1365 1363 1361 1359 1357 1355 1353 1351 1349 1347 1345 1343 1341 1339 1337 1335 1333 1331 1329 1327 1325 1323 1321 1319 1317 1315 1313 1311 1309 1307 1305 1303 1301 1299 1297 1295 1293 1291 1289 1287 1285 1283 1281 1279 1277 1275 1273 1271 1269 1267 1265 1263 1261 1259 1257 1255 1253 1251 1249 1247 1245 1243 1241 1239 1237 1235 1233 1231 1229 1227 1225 1223 1221 1219 1217 1215 1213 1211 1209 1207 1205 1203 1201 1199 1197 1195 1193 1191 1189 1187 1185 1183 1181 1179 1177 1175 1173 1171 1169 1167 1165 1163 1161 1159 1157 1155 1153 1151 1149 1147 1145 1143 1141 1139 1137 1135 1133 1131 1129 1127 1125 1123 1121 1119 1117 1115 1113 1111 1109 1107 1105 1103 1101 1099 1097 1095 1093 1091 1089 1087 1085 1083 1081 1079 1077 1075 1073 1071 1069 1067 1065 1063 1061 1059 1057 1055 1053 1051 1049 1047 1045 1043 1041 1039 1037 1035 1033 1031 1029 1027 1025 1023 1021 1019 1017 1015 1013 1011 1009 1007 1005 1003 1001 999 997 995 993 991 989 987 985 983 981 979 977 975 973 971 969 967 965 963 961 959 957 955 953 951 949 947 945 943 941 939 937 935 933 931 929 927 925 923 921 919 917 915 913 911 909 907 905 903 901 899 897 895 893 891 889 887 885 883 881 879 877 875 873 871 869 867 865 863 861 859 857 855 853 851 849 847 845 843 841 839 837 835 833 831 829 827 825 823 821 819 817 815 813 811 809 807 805 803 801 799 797 795 793 791 789 787 785 783 781 779 777 775 773 771 769 767 765 763 761 759 757 755 753 751 749 747 745 743 741 739 737 735 733 731 729 727 725 723 721 719 717 715 713 711 709 707 705 703 701 699 697 695 693 691 689 687 685 683 681 679 677 675 673 671 669 667 665 663 661 659 657 655 653 651 649 647 645 643 641 639 637 635 633 631 629 627 625 623 621 619 617 615 613 611 609 607 605 603 601 599 597 595 593 591 589 587 585 583 581 579 577 575 573 571 569 567 565 563 561 559 557 555 553 551 549 547 545 543 541 539 537 535 533 531 529 527 525 523 521 519 517 515 513 511 509 507 505 503 501 499 497 495 493 491 489 487 485 483 481 479 477 475 473 471 469 467 465 463 461 459 457 455 453 451 449 447 445 443 441 439 437 435 433 431 429 427 425 423 421 419 417 415 413 411 409 407 405 403 401 399 397 395 393 391 389 387 385 383 381 379 377 375 373 371 369 367 365 363 361 359 357 355 353 351 349 347 345 343 341 339 337 335 333 331 329 327 325 323 321 319 317 315 313 311 309 307 305 303 301 299 297 295 293 291 289 287 285 283 281 279 277 275 273 271 269 267 265 263 261 259 257 255 253 251 249 247 245 243 241 239 237 235 233 231 229 227 225 223 221 219 217 215 213 211 209 207 205 203 201 199 197 195 193 191 189 187 185 183 181 179 177 175 173 171 169 167 165 163 161 159 157 155 153 151 149 147 145 143 141 139 137 135 133 131 129 127 125 123 121 119 117 115 113 111 109 107 105 103 101 99 97 95 93 91 89 87 85 83 81 79 77

	361	375	376	390	391	405	406	420	421	435	436	450
2 STEAP2	IEMLISFGIMSLGIL	SLLAATSPSPSVSNAL	NWREFSFIOSTLGYV	ALLISTFHVLYGNK	RAFESEYVRYATPPN	FVLAIVLE	-SIVILD					445
3 STEAP3	SDSVAALGEGFFLF	VHIGITSEPSVSNV	NWREFRFVOSKLGYL	TILCDAHTLVGCK	RFLSPSNLRWYLPAA	YVIGLIIIPCTVLVIR						434
4 STEAP1	MEENVSIGTVGLAID	AGLAATSIPIPSVSDSI	TNREHYIQSKLGIV	SHLGGIHALIFAWN	KWIDIKQFVWYPPPT	EMIAVFERIVVEEFK						305
5 STEAP4	MEKYLSLGVIALGTT	SLIAVNSPIPSIANSL	NWREFSFVQSSLGIV	AXVLSLHTIYGT	RAFESERYKEVLPPT	FTXTLVF	-QVRSSW					120

	451	465	466	480	481
2 STEAP2	LLQICRYPD				454
3 STEAP3	FVGIIMPQVDNTLTR	ROGWERNSKH			459
4 STEAP1	SIFFLPCLRKILKE	RHGVEDVTINKTEI	CSQL		339
5 STEAP4	AKAFEXLECIQPX				133

FIG. 11B

STRAP-1	67	LFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLEPMVSITLL
STRAP-2	208	LFTLWRGPVVVAISLATFFFLYSEFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLL
		*** *
STRAP-1	127	ALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFVAVLHAIYSLSPMRR
STRAP-2	268	SLVYLACLLAAAYQLYYGTKYRRFPWLETWLQCRKQLGLLSFFFAMVHVAYSICLPMRR
		*** *
STRAP-1	187	SYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLT
STRAP-2	328	SERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALN
		* *
STRAP-1	247	WREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLI
STRAP-2	388	WREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYRFYTPPNFVLALVLPISIVL
		*** *

FIG. 11C

STEAP1 66 ELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMSITL

STEAP3 195 QLFPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTL
*** * * * * * * * *

STEAP1 126 LALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMR

STEAP3 255 LALVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIR
***** ** ***** ** * * * * *

STEAP1 186 RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSL

STEAP3 315 YYVRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLSVSNV
* * * * * * * * * *

STEAP1 246 TWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIFK

STEAP3 375 NWREFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAAYVLGLIIPCTVLVIK
***** * * * * * * * *

STEAP1 306 SILFLPCLRKKILKIRHGWEDVTK

STEAP3 435 FVLIMPCVDNTLTRIRQGWERNK
* * * * *

FIG. 11D

STEAP2 29 RKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTKTNI

STEAP3 18 KQETVCIFGTGDFGRSLGLKMLQCGYSVVFGSRNPQ-KTTLLPSGAEVLSYSEAAKSGI
* * * * *

STEAP2 89 IFVAIHREHYTSLWDLRHLLVGKILIDVSNMNRINQYPESNAEYLAFLPDSLIVKGFNV

STEAP3 77 IIIAIIHREHYDFLTEVLTNGKILVDISNNLKINQYPESNAEYLAHLVPGAHVVKAFNT
* * * * *

STEAP2 149 VSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGLSSAREIENLPLRL

STEAP3 137 ISAWALQSGALDASRQVFVCGNDSKAKQRMVMDIVRNGLTPMDQGSMAAKEIEKYPLQL
* * * * *

STEAP2 209 FTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPPIVAITLLS

STEAP3 197 FPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTLLA
* * * * *

STEAP2 269 LVYLAGLLAAAYQLYYGTKYRRFPWLETWLQCRKQLGLLSFFFAMVHVAYSLLCLPMRRS

STEAP3 257 LVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVPIPIRY
* * * * *

STEAP2 329 ERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNW

STEAP3 317 VRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLSVSNVNW
* * * * *

STEAP2 389 REFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYRFTPPNFVLALVLPISIVIL

STEAP3 377 REFRFVQSKLGYLTLLCTAHTLVYGGKRFLSPSNLRWYLPAAVVLGLIIPCTVLV
* * * * *

FIG. 12A

Panel 1.

Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas

Panel 2.

Spleen
Thymus
Prostate
Testes
Ovary
Small Intestine
Colon
White Blood Cell

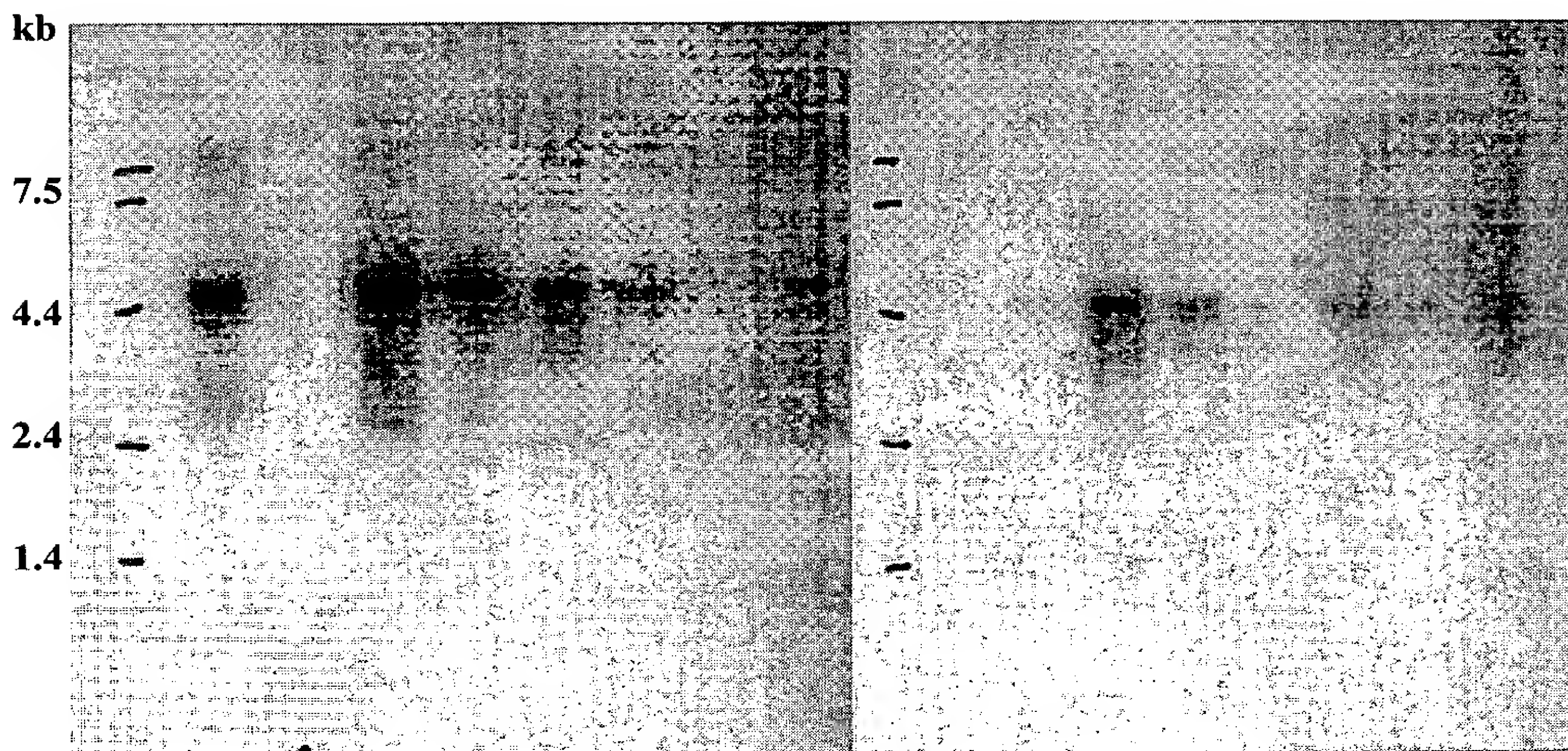
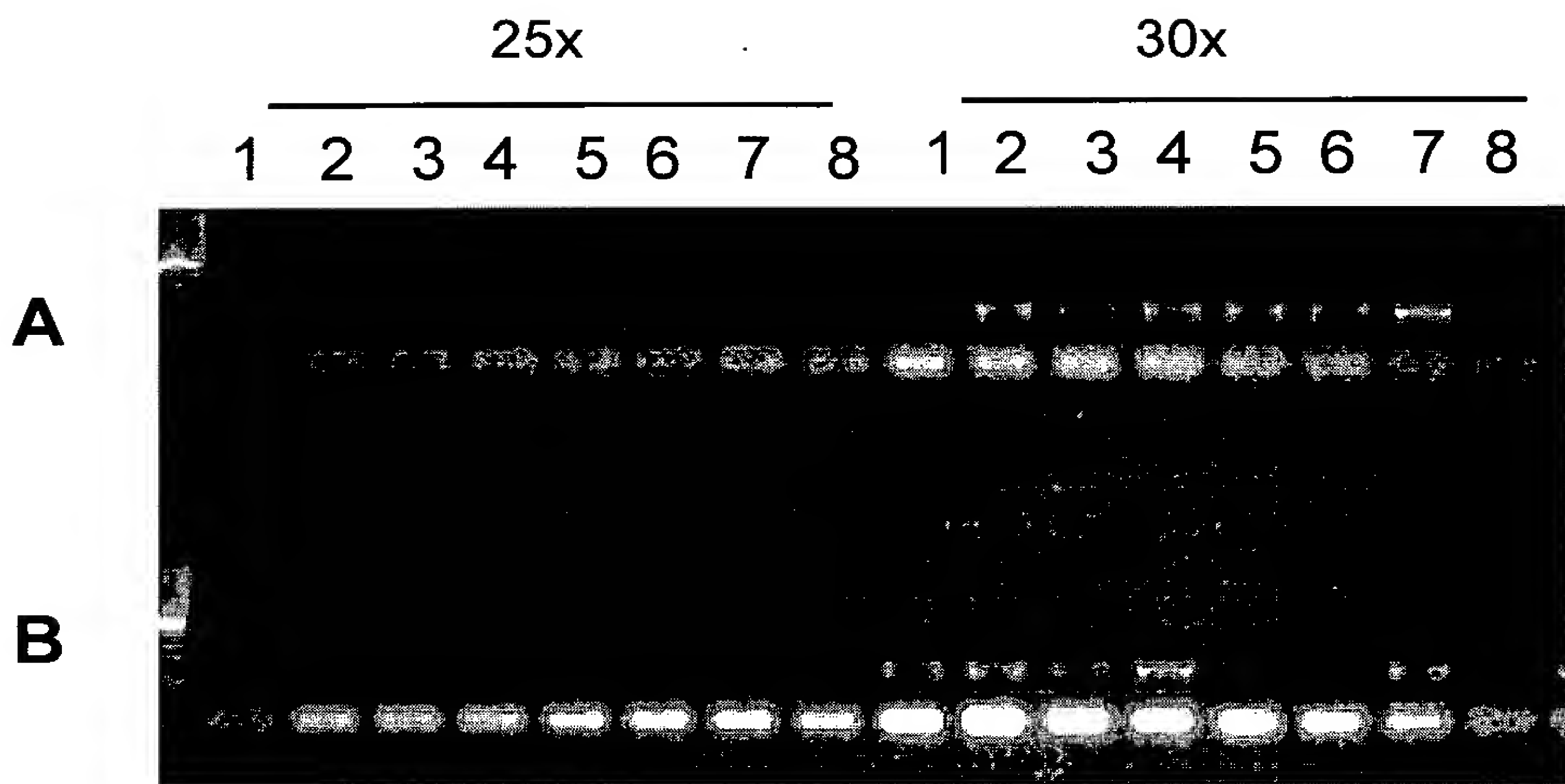


FIG. 12B



A

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

B

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

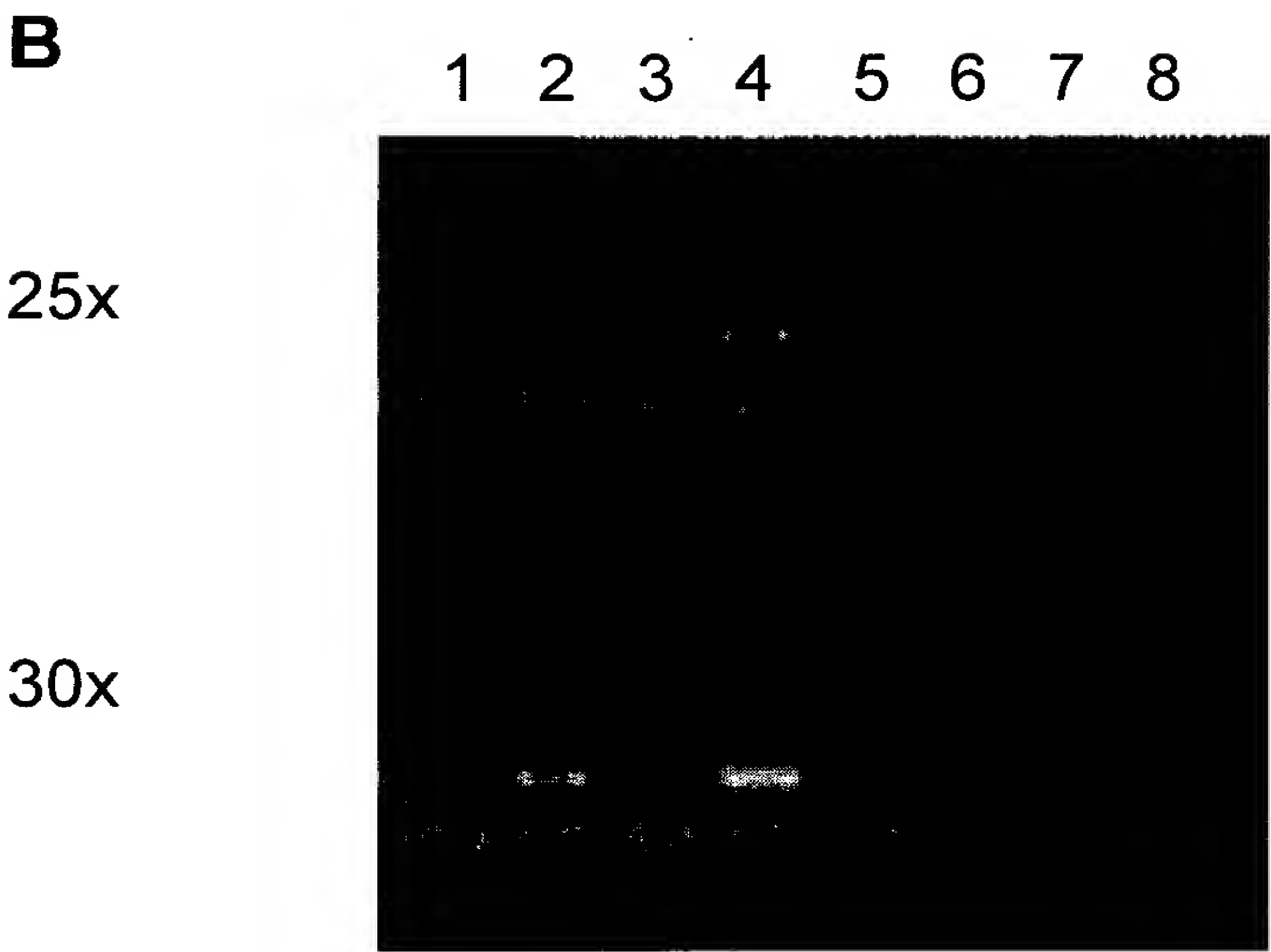
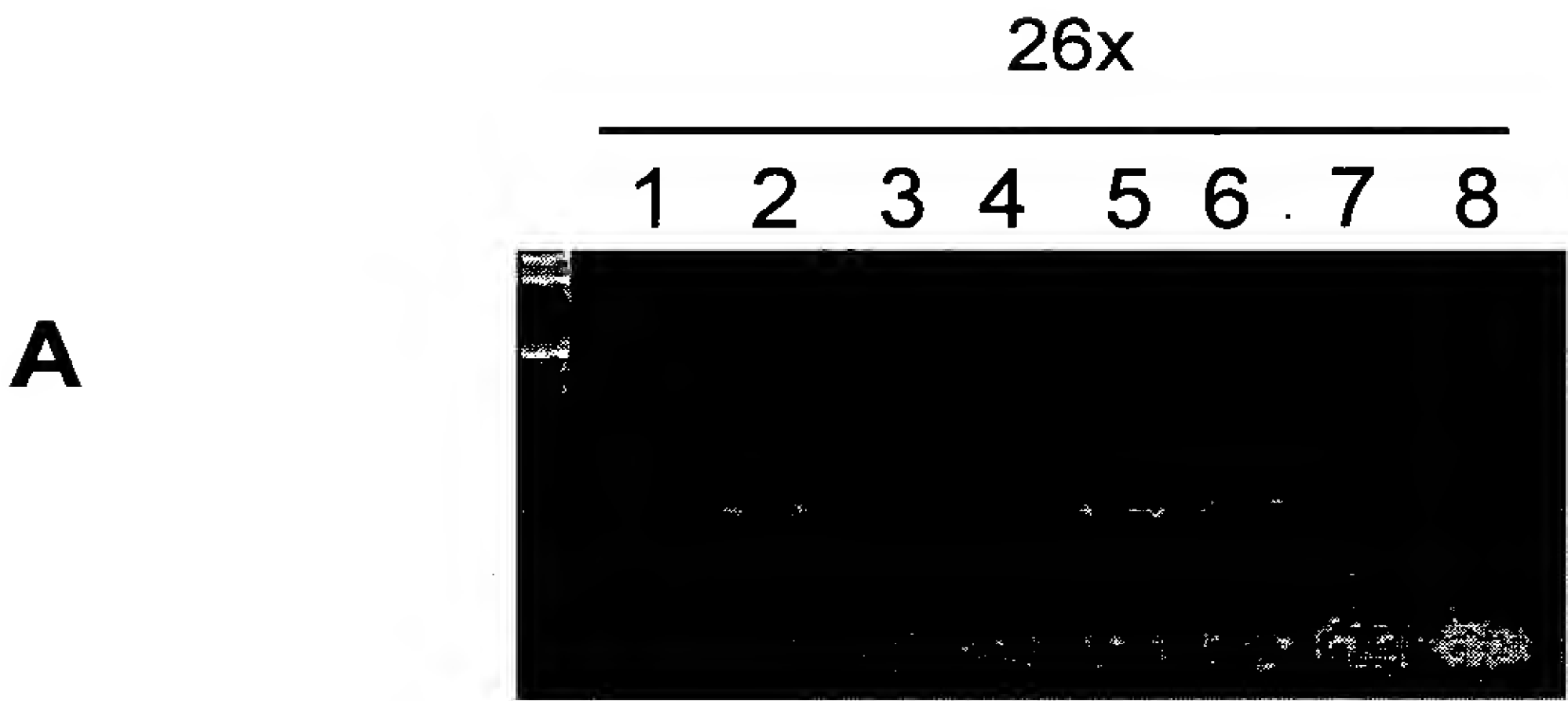
B



- B**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG.14



- A**
- 1. Brain
 - 2. Prostate
 - 3. LAPC-4 AD
 - 4. LAPC-4 AI
 - 5. LAPC-9 AD
 - 6. HeLa
 - 7. Murine cDNA
 - 8. Neg. control

- B**
- 1. Colon
 - 2. Ovary
 - 3. Leukocytes
 - 4. Prostate
 - 5. Small Intestine
 - 6. Spleen
 - 7. Testis
 - 8. Thymus

FIG. 15

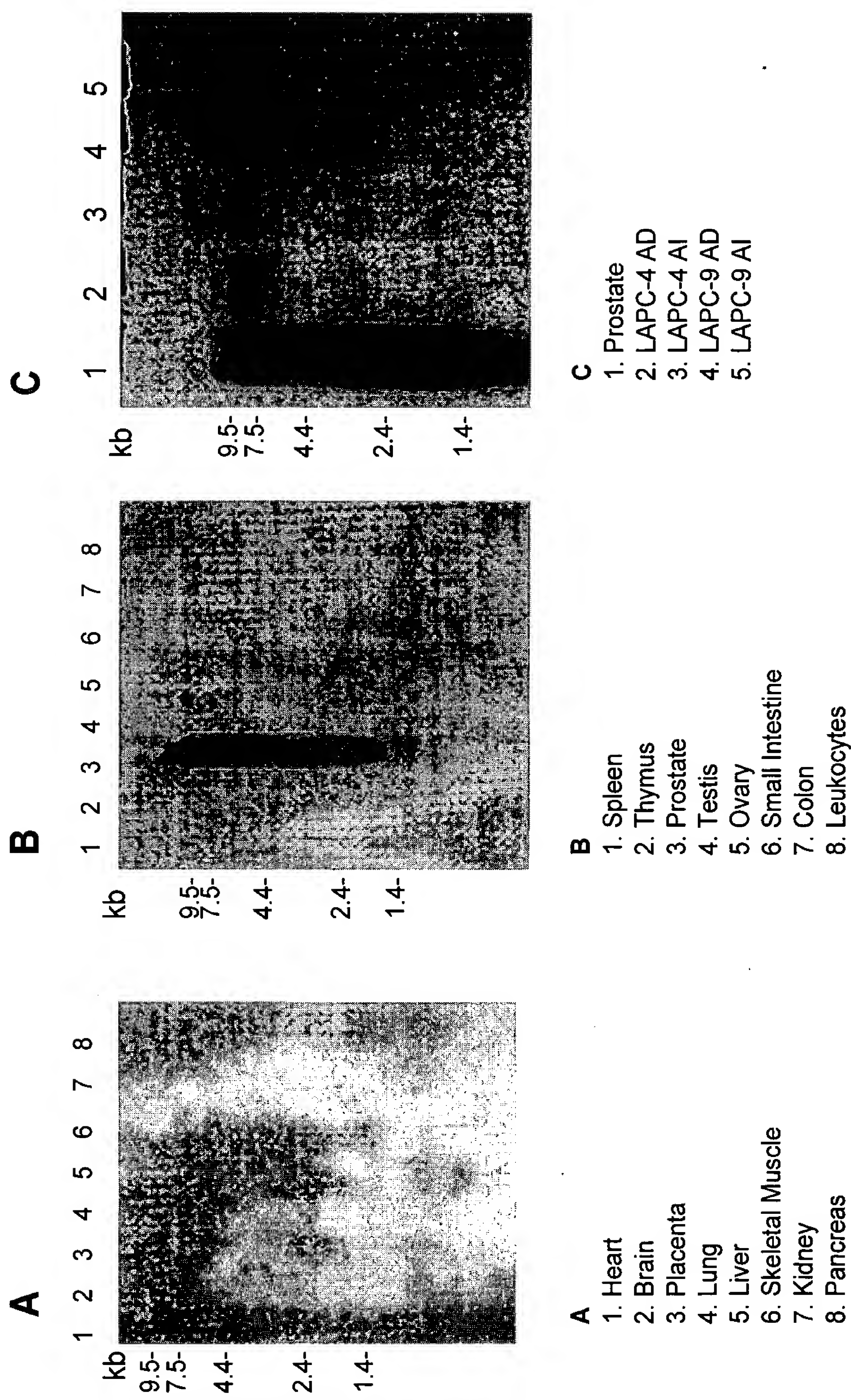


FIG. 16

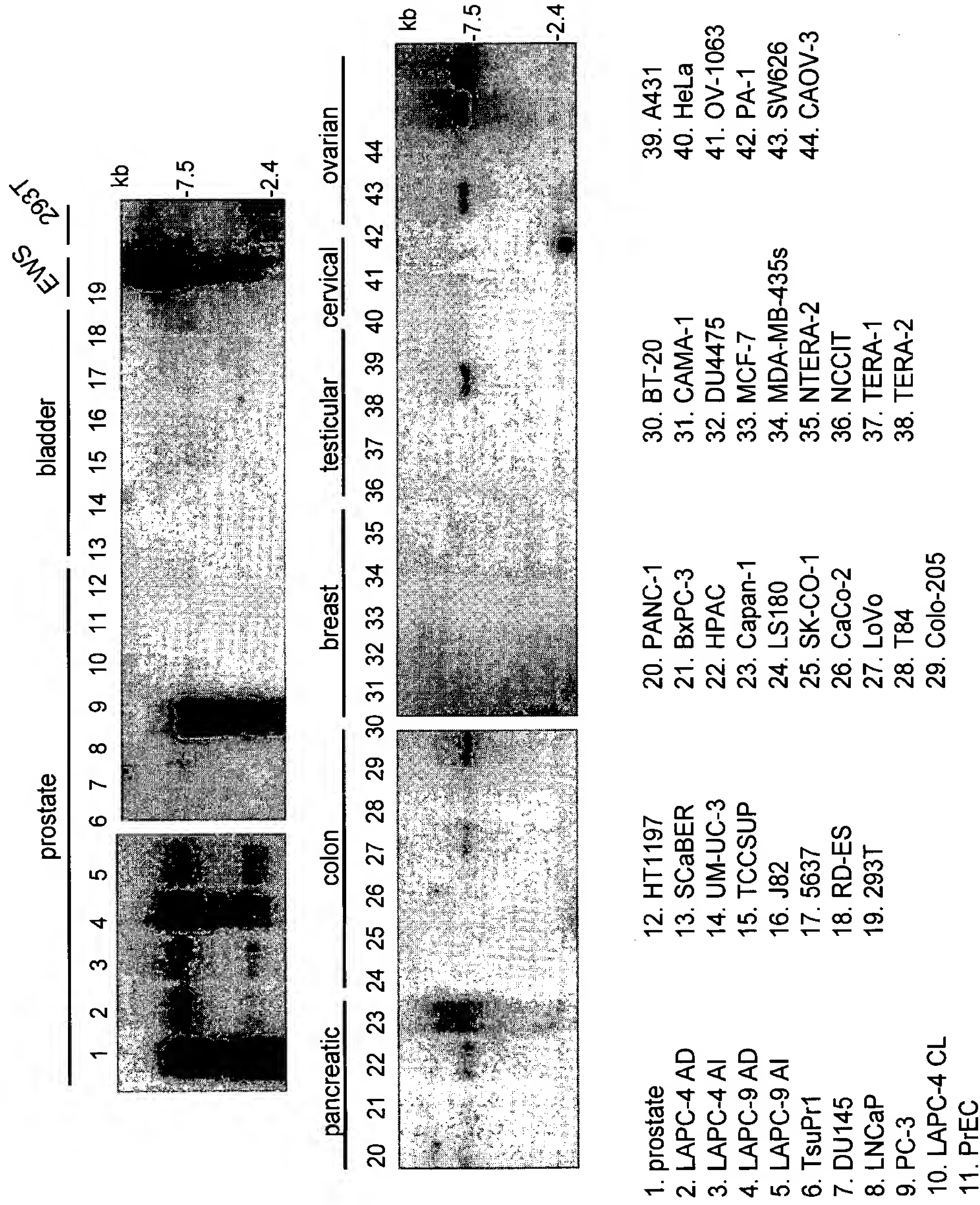


FIG. 17

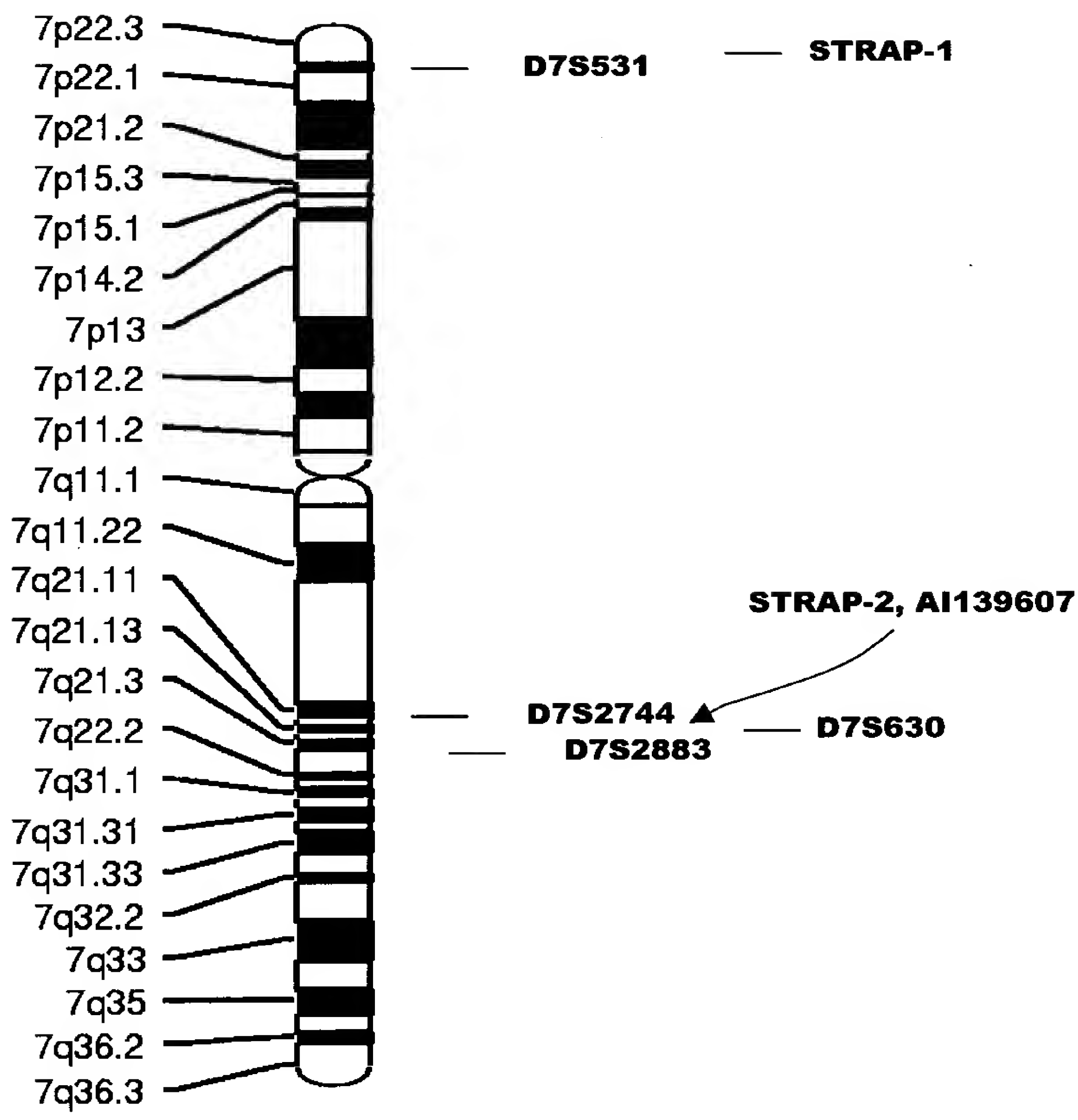


FIG. 18

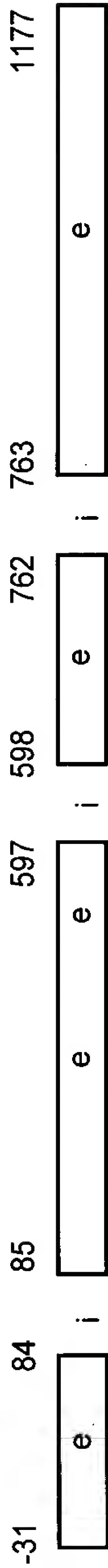


FIG. 19

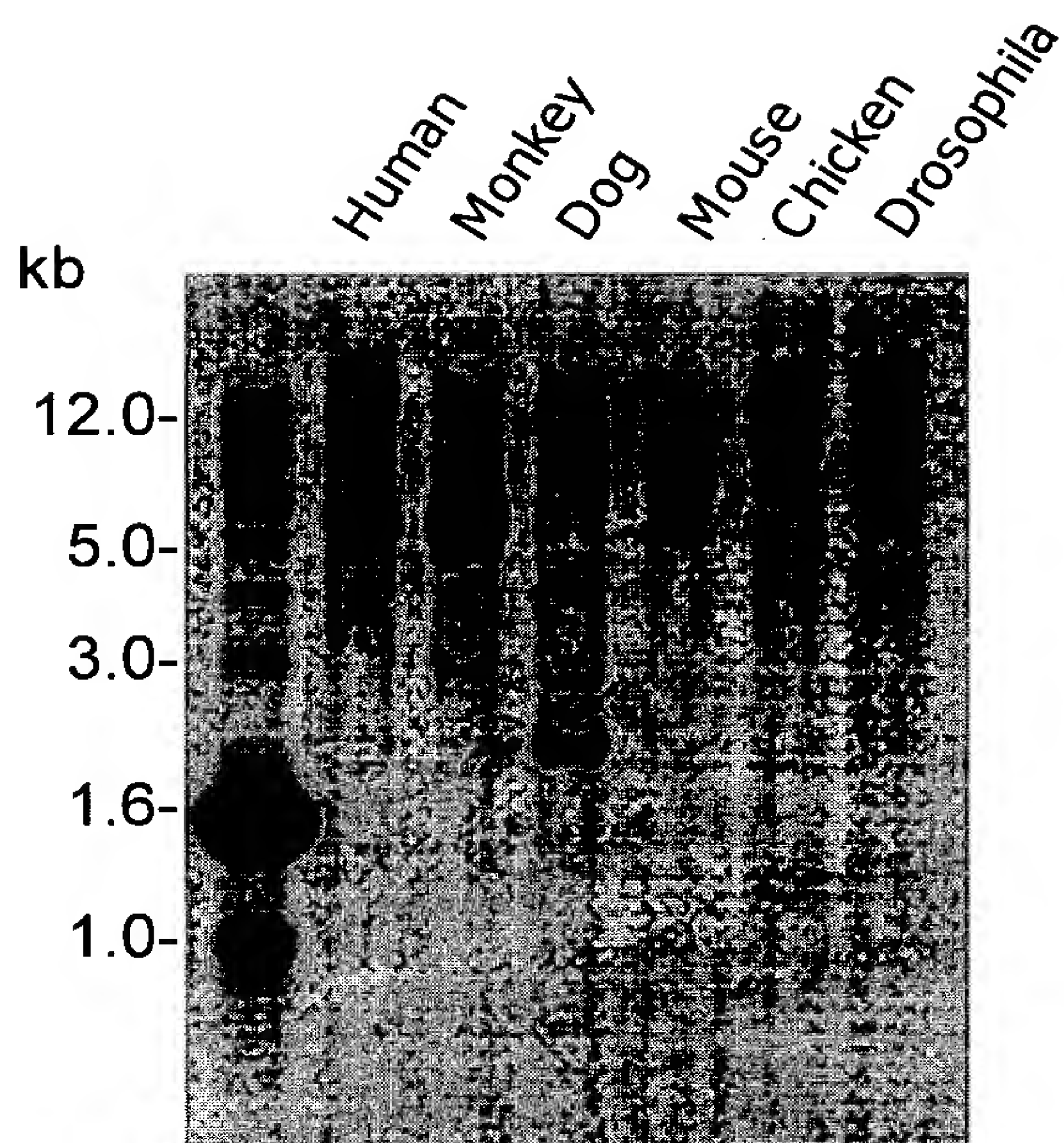
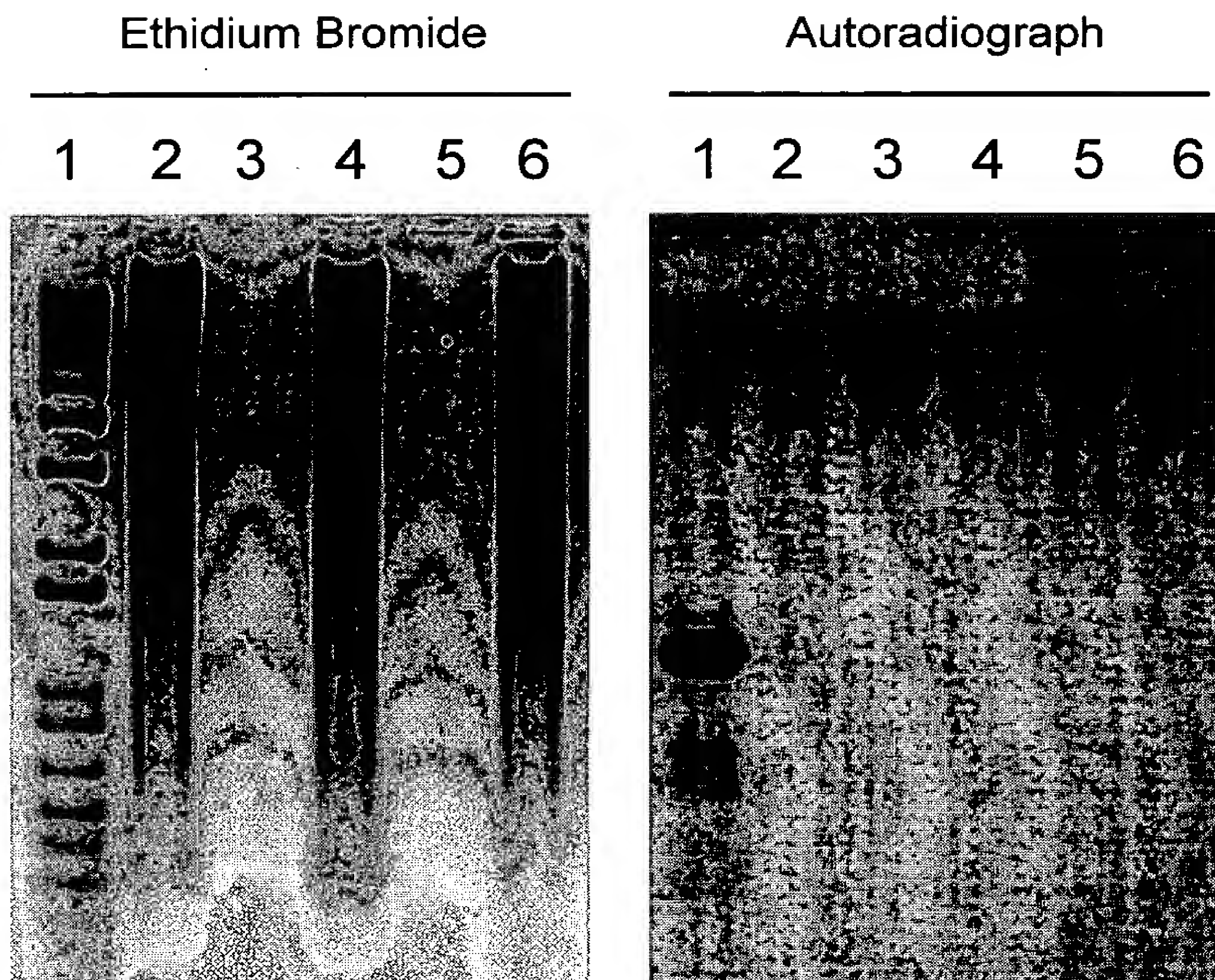


FIG. 20



Lanes

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3